

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:  
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

Page 60 of 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 97.0088 Seconds  
(without alignments)  
1374.564 Million cell updates/sec

Title: US-09-811-367b-1  
Perfect score: 1023  
Sequence: 1 MTDSVIYSMLPLPTAQON.....GLQASSCEVPLHGCKKAVRL 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_05.80:.\*  
2: uniprot\_sprot:.\*  
3: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	2	043198_HUMAN
2	1007	98.4	189	2	075613_HUMAN
3	548.5	53.6	188	2	088713_MOUSE
4	525.5	51.4	188	2	064335_RAT
5	170.5	16.7	188	2	062YP6_CHICK
6	168.5	16.5	188	2	062YP3_CHICK
7	159	15.5	188	1	CLCSA_HUMAN
8	131.5	12.9	189	2	052M11_HUMAN
9	131.5	12.9	189	2	08C634_MOUSE
10	126	12.3	189	2	061969_MOUSE
11	106.5	10.4	188	2	096DB9_HUMAN
12	103.5	10.1	188	2	09W012_DROME
13	96.5	9.4	189	2	060S03_CAEBR
14	92.5	9.0	188	2	09T275_CAEBL
15	82.5	8.1	189	2	018202_CAEBL
16	72.5	7.1	188	2	09W108_DROME
17	69	6.7	188	2	09MF32_GUCU
18	67	6.5	189	2	09MF30_GUCU
19	66.5	6.5	188	2	07K7K8_CAEBL
20	65.5	6.4	189	2	086129_MYTB
21	60.5	5.9	188	2	0814K8_CAEBL
22	60.5	5.9	188	2	07PLU0_DROME
23	58	5.7	188	2	030134_ARCTU
24	58	5.7	189	2	023831_PCRYT
25	58	5.7	189	2	075UD3_DICDI
26	57.5	5.6	188	2	04UHL7_THEAN
27	57	5.6	188	2	028946_PIG
28	57	5.6	188	2	06MKR9_BDEBA
29	57	5.6	189	2	08W0R0_GCRYT
30	56	5.5	189	2	08UWS9_CHICK
31	55.5	5.4	188	1	V060_FOWPV

32	55.5	5.4	188	2	06UDX7_9DIPR	061dx7 cuterebra f
33	55.5	5.4	188	2	070H91_FOWPV	070h91 fowlox vir
34	55.5	5.4	188	2	04SYA7_TETNG	04syat tetrapox vir
35	55.5	5.4	189	2	06ZRB9_HUMAN	06zrb9 homo sapien
36	55.5	5.4	189	2	09XXB7_CAEBL	09xxb7 caenorhabdi
37	55.5	5.4	189	2	04RSS5_TETNG	04rss5 tetrapox n
38	55.5	5.4	188	2	054V41_DICDI	054v41 dictyostell
39	55	5.4	188	2	068P15_CPNSC	068p15 centruroid
40	55	5.4	188	2	04YFS2_PLABE	04yfs2 plasmodium
41	55	5.4	188	2	05N2Z5_AZOSE	05n2z5 azoarcus sp
42	54.5	5.3	189	1	E321_ADEB7	P15138 human adeno
43	54.5	5.3	189	2	05MD81_9DIPR	05md81 diplochora
44	54.5	5.3	189	2	09PE95_XYLEFA	09pe95 xyella fas
45	54.5	5.3	189	2	05EY51_ADEB7	05ey51 human adeno

## ALIGNMENTS

RESULT 1	043198_HUMAN	PRELIMINARY;	PRT;	189 AA.
ID	043198_HUMAN	PRELIMINARY;	PRT;	189 AA.
AC	043198;			
DT	01-JUN-1998	(TREMBLrel. 06, Created)		
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Maat cell function-associated antigen.			
GN	Name=MAFA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Enzyme digested lung;			
RX	MEDLINE=98438735, PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;			
RT	"Human MAFa has alternatively spliced variants."			
RL	Biochim. Biophys. Acta 1399:209-212 (1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Enzyme digested lung;			
RA	Lamers M.B.A.C., Lamont A.G., Williams D.H.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF034952; AAC34731.1; -; mRNA.			
DR	HSSP; Q13241; 1B6E.			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	GO; GO:0004872; F:receptor activity; TAS.			
DR	GO; GO:0005229; F:sugar binding; TAS.			
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.			
DR	GO; GO:0006968; P:cellular defense response; TAS.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	InterPro: IPR001304; Lectin_C.			
DR	Pfam; PF00059; Lectin_C_1.			
DR	SMART; SM00034; CUECT_1.			
DR	PROSITE; PSS0041; C-TYPE_LECTIN_2, 1.			
DR	SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;			
QY	Query Match	100.0%;	Score 1023;	DB 2; Length 189;
QY	Best Local Similarity	100.0%;	Pred. No. 2, 7e-89;	
QY	Matches 189;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MTDSVIYSMLPLPTAQNDYGPQKSSSKPSCGLVAITIGLTLAVLLSVLLYMWL	60	
QY	1	MTDSVIYSMLPLPTAQNDYGPQKSSSKPSCGLVAITIGLTLAVLLSVLLYMWL	60	
QY	61	COGSNSTCASCPSCPDPMKYGKHCYFVEEKDMNSLFCPLARDSHLLVITDNOEMS	120	
QY	61	COGSNSTCASCPSCPDPMKYGKHCYFVEEKDMNSLFCPLARDSHLLVITDNOEMS	120	
QY	61	COGSNSTCASCPSCPDPMKYGKHCYFVEEKDMNSLFCPLARDSHLLVITDNOEMS	120	
QY	121	LLQVFLSEAFQWIGLRNNSGMRWEDGSLPLFSRISNSFVQTGALINKGSLQASSCEVPL	180	
QY	121	LLQVFLSEAFQWIGLRNNSGMRWEDGSLPLFSRISNSFVQTGALINKGSLQASSCEVPL	180	

```

Db      121 LLQVFLSEAFWIGLIRNNSGMRWEDGSPINFSRISNSFVQTCAINKGLQASSCEVPL 180
Qy      181 HGVCKKVRLL 189
Db      181 HGVCKKVRLL 189

RESULT 2
075613 HUMAN
ID      075613_HUMAN PRELIMINARY; PRT; 189 AA.
AC      075613;
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT      01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE      ITIM-containing receptor MARA-L (Mast cell function-associated antigen
DE      ho40log).
GN      Name=MARF;
OS      Homo sapiens (Human).
OC      Mammalia; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo
OC      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99057052; PubMed=9842918;
RX      DOI=10.1002/(SICI)1521-4141(199811)28:11<3755::AID-IMMU3755>3.0.CO;2-3;
RA      Butcher S., Arney K.L., Cook G.P.;
RT      "MARA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT      complex and expressed by basophils and NK cells.";
RL      Eur. J. Immunol. 28:3755-3762(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99077194; PubMed=9862378;
RA      Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT      "2F1 antigen, the mouse homolog of the rat 'mast cell function-
RT      associated antigen', is a lectin-like type II transmembrane receptor
RT      expressed by natural killer cells.";
RL      Eur. J. Immunol. 28:4409-4417(1998).
DR      EMBL; AF081675; AAC3200.1; -; mRNA.
DR      EMBL; AF097358; AAD03719.1; -; mRNA.
DR      HSSP; Q13241; 1B6E.
DR      GO; GO:004872; F:receptor activity; IEA.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; Lectin_C.1.
DR      SMART; SM00034; CLECT_1.
DR      PROSITE; P550041; C_TYPE_LECTIN_2; 1.
KW      Receptor.
SQ      SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match      98.4%; Score 1007; DB 2; Length 189;
Best Local Similarity 98.4%; Pred. No. 9,2e-88;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

ID      088713_MOUSE PRELIMINARY; PRT; 188 AA.
AC      088713;
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT      10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE      Mast cell function-associated antigen 2F1 (killer cell lectin-like
DE      receptor G1) (MARF).
GN      Name=Klrg1; Synonyms=Mafa; mafa;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OC      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C.B-17 SCID;
RX      MEDLINE=99077194; PubMed=9862378;
RA      Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT      "2F1 antigen, the mouse homolog of the rat 'mast cell function-
RT      associated antigen', is a lectin-like type II transmembrane receptor
RT      expressed by natural killer cells.";
RL      Eur. J. Immunol. 28:4409-4417(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX      MEDLINE=21115136; PubMed=11220622; DOI=10.1007/s002510000282;
RA      Voeltinger D., Kaufmann M., Pircher H.;
RT      "Genomic structure, alternative splicing, and physical mapping of the
RT      killer cell lectin-like receptor G1 gene (Klrg1), the mouse homologue
RT      of MARF.";
RL      Immunogenetics 52:206-211(2001).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99077501; PubMed=9862665;
RA      Blaser C., Kaufmann M., Pircher H.;
RT      "Virus-activated CD8 T cells and lymphokine-activated NK cells express
RT      the mast cell function-associated antigen MARF, an inhibitory C-type
RT      lectin.";
RL      J. Immunol. 161:6451-6454(1998).
DR      EMBL; AF097357; AAD03718.1; -; mRNA.
DR      EMBL; AF317727; AAK40082.1; -; Genomic_DNA.
DR      EMBL; AJ010751; CAA09342.1; -; mRNA.
DR      HSSP; Q13241; 1B6E.
DR      Ensemble; ENSMUSG0000030114; Mus musculus.
DR      MGI; MGI:1355294; Klrg1.
DR      GO; GO:0016021; C:integral to membrane; TAS.
DR      GO; GO:0005529; F:sugar binding; TAS.
DR      GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; Lectin_C.1.
DR      SMART; SM00034; CLECT_1.
DR      PROSITE; P550041; C_TYPE_LECTIN_2; 1.
KW      Lectin; Receptor.
FT      CHAIN 2 188 mast cell function-associated antigen
FT      (MARF).
SQ      SEQUENCE 188 AA; 21396 MW; 876336802EAJ34F1 CRC64;

Query Match      53.6%; Score 548.5; DB 2; Length 188;
Best Local Similarity 55.6%; Pred. No. 4.5e-44;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

```

RESULT 3  
088713\_MOUSE



```

Oy      181 HGVCCKV 187      :||||
Db      180 QWICKV 186
RESULT 4
064335 RAT
AC Q64335 PRELIMINARY; PRT: 188 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, last annotation update)
DE MAFPA protein (mast cell function associated antigen).
GN Name=Klrg1; Synonyms=MAFA, mata;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley; TISSUE=Testis;
RX MEDLINE=97240766; PubMed=9120279;
RA Bocek Jr P., Guhmann M.D., Pecht I.;
RT Analysis of the gene encoding the mast cell function-associated
RT antigen and its alternatively spliced transcripts."
RT J. Immunol. 158:3235-3243(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96016176; PubMed=7568140;
RA Guhmann M.D., Tai M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RT another C-type lectin."
RT Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL: X97191; CAA65829.1; -; Genomic_DNA.
DR EMBL: X79812; CAA65208.1; -; mRNA.
DR EMBL: X97192; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL: X97193; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL: X97194; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL: X97195; CAA65829.1; JOINED; Genomic_DNA.
DR PIR: I59421; I59421.
DR HSSP: P26718; 1KCG.
DR Ensemble; ENSKNOG0000014918; Rattus norvegicus.
DR RGD; 61978; Klrg1.
DR GO; GO:000529; F:sugar binding; IEA.
DR InterPro; IPR01304; Lectin_C.
DR Pfam; PF00059; Lectin_C_1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2, 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032AD020B15 CRC64;
Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 6.9e-42;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1
Oy      1 MTDSVIYSMLELPTATOAQNDYGPQOKSSSRKSCSVATITGLITLAVLSVLLYQWIL 60
Db      1 MADNSIYITLELPAPPRVQDDSRMKVYKVLHRPCVSYLVMLGLITVIMSLILLYQRTL 60
Oy      61 CGGSNYSTCASCPCPDPRMKYGNHCYFVSVEKQWNSLEFCLARDSHLVITTDQMS 120
Db      61 CCGSGKGFMCSCQSRCPNLIMRNGSHCYFYSMKRQWNSLKFCAKGGSHLTFPPNOGVN 120
Oy      121 LLQVFLSEAFPCWITGIRNNSGMRWEGSSPLNFSRISNSVPCGAIINKKGLQASSCEVPL 180
Db      121 LPEQVEDEFPYITGLRIDIDGMRWEDGSPALSLT-ILSNSVQKCGTITHRGGLAASSCEVAL 179
Oy      181 HGVCCKV 187      :|:|
Db      180 QWICKV 186
RESULT 5

```

ID	Q6ZYP6_CHICK PRELIMINARY;	PRT;	188 AA.
AC	Q6ZYP6_		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	B-1ec protein.		
GN	Name=B-1ec;		
OS	Gallus gallus (chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Bone marrow;		
RX	PubMed=15749883;		
RA	Rogers S.L., Gobel T.W., Vierlboeck B.C., Milne S., Beck S.,		
RA	Kaufman J.;		
RT	"Characterisation of C-type lectin-like receptors B-NK and B-1ec		
RT	reveals that the NK Complex and the MHC share a common ancestral		
RT	region.";		
RL	J. Immunol. 174:3475-3483(2005).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Bone marrow;		
RA	Rogers S.L.;		
RT	"Characterisation of C-type lectin-like receptors in the chicken		
RT	MHC.";		
RL	Thesis (2002), Department of Pathology and Microbiology, University of		
RL	Bristol, Bristol, United Kingdom.		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Bone marrow;		
RA	Kaufman J.F.;		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ634334; CAG25418.1; -; mRNA.		
DR	HSPB, Q9H8P0; 1K9J.		
DR	GO; GO:0005529; F:sugar binding; IEA.		
DR	InterPro; IPR002353; AntiFreezeII.		
DR	InterPro; IPR001304; Lectin_C.		
DR	Pfam; PF00059; Lectin_C.1.-		
DR	PRINTS; PR00356; ANTIFREEZEII.		
DR	SMART; SM00034; CLECT.1.		
DR	PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.		
DR	PROSITE; PS50041; C_TYPE_LLECTIN_2.1.		
DR	SEQUENCE 188 AA; 20397 MW; 9F5BD2D9BF9FE41 CRC64;		
Query Match	16.7%;	Score 170.5;	DB 2; Length 188;
Best Local Similarity	27.3%;	Pred. No. 4.7e-08;	
Matches	48; Conservative 24; Mismatches 77;	Indels 27; Gaps 6	
QY	26 OKSSSSKSC-----SCLVATTLGLTAVLVLSVLTYQWILCGSNYSTCASCSPCDRWM 80		
Db	17 RREGSGRACVTPQLTMAAVFTVLITVAFAVQAFQ-----PHQPCACPFDWI 67		
QY	81 KYGNHCYFYSVEKQWNSLSEFCIARDSHLVITDQMSLQVLSAFCIGIRNNS- 139		
Db	68 GPRGCTCYFSEDSNWTSSQNCCSLGASLAVFDSABDLFTMRKGSPPHWGLSRECK 127		
QY	140 --GAWWEGSPINFRISNSF-VQ---TCGAINKNGIQAASCVEPLGVCKKVR 189		
Db	128 EHWMEWVRSP-----SHLFQVQGDGLCAVLGADGLSSHCARRNVCCKPAL 177		
RESULT 6			
ID	Q6ZYP3_CHICK PRELIMINARY;	PRT;	188 AA.
AC	Q6ZYP3_		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	B-1ec protein.		

```

GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Bursa;
RX PubMed=1579883;
RA Rogers S.L., Gobel T.W., Viertlboeck B.C., Milne S., Beck S.,
RA Kaufman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Bursa;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC.";
RL Thesis (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Bursa;
RA Kaufman J.F.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ634337; CAG25421.1; -; mRNA.
DR HSP; O9H8F0; 1k97.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro: IPR002353; Antifreeze21.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR SMART; SM00364; ANTI-FREEZE21.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21053 MW; 6AD5AC9CB8F440 CRC64;

Query Match 16.5%; Score 168.5; DB 2; Length 188;
Best Local Similarity 27.3%; Pred. No. 7.3e-08;
Matches 48; Conservative 24; Mismatches 77; Indels 27; Gaps 6;

QY 26 QSSSSSKPSC-----SCLVAITLGLTAVLISVLYQWILCGSNYSTCASCSPCPDRM 80
DB 17 RREGPSRGACVTFQLTMAAVFTVLLITVAFAVQAFQ-----PHPOCAQCPDWI 67
QY 81 KYGNHCYFYSVEEKDNSSLEFCLARDSHLITDQEMSLIQVLEAFICWIGLRNNS- 139
DB 68 GRGKCYFSEDESNWTSQNNCSALGASLAFDSDSEDSFTMRKKGSPHVGSLRBEK 127

QY 140 --GWRWEDGSPINFSRISNSF-VQ--TCGAINKNGIQAASSCEVPLHGVCCKVRL 189
DB 128 EHPMEWVNSPL-----SHLFQVQDGLCAVIGDAGLSSSHCSRFRMNVCTKPAL 177

RESULT 7
ID CLC5A HUMAN STANDARD; PRT; 188 AA.
AC O9NY25; O9UK00;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type lectin domain family 5 member A (C-type lectin superfamily
DE member 5) (Myeloid DAP12-associating lectin) (MDL-1).
GN Name=CLC5A; Synonyms=CLEC5A, MDL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,
RP INTERACTION WITH TYROBP, AND MUTAGENESIS OF LYS-16.
RX MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;
RA Baker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
RA "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Mueller A., Metz H., Feller A.C.;
RT "Expression of MDL-1 in human blood and cell lines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Biellack L., Scott K., Holmes A., Harting R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesener J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speith J.,
RA Bieri T.A., Nelson J.O., Berkowitz N., Wohlmann P.E., Cook L.L.,
RA Hickenoatham M.T., Eldred J., Williams D., Bedell J.A., Mardis B.R.,
RA Clifton S.W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb E.,
RA Stims E., Levy R., Clendenning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterson R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
CC -1- FUNCTION: May be involved in proinflammatory activation of myeloid
CC cells via TYROBP-mediated signaling in a calcium-dependent manner.
CC -1- SUBUNIT: Interacts with TYROBP.
CC -1- TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in
CC cell lines of other origins. Expression is down-regulated when
CC monocytes differentiate into dendritic cells.
CC -1- SIMILARITY: Contains 1 C-type lectin domain.
CC This Swiss-Prot entry is copy-right. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: AF139768; AAF02491.1; -; mRNA.
CC EMBL: AJ271684; CAB71334.1; -; mRNA.
CC EMBL: AC073647; AAS07444.1; -; Genomic_DNA.
CC HSP; P22897; IE63.
CC Ensembl: ENSG00000090269; Homo sapiens.
CC HGNC: HGNC:2054; CLC5A.
CC MIM: 604987; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005488; F:binding; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro: IPR002353; Antifreeze21.

```

InterPro: IPR001304; Lectin\_C.  
DR Pfam: PF00059; Lectin\_C; 1.  
DR PRINTS: PR00356; ANTI\_FERREZII.  
DR SMART: SM00034; CLECT; 1.  
DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
DR PROSITE: PS00641; C\_TYPE\_LECTIN\_2; 1.  
KW Alternative splicing; Glycoprotein; Immune response; Lectin;  
KW Signal-anchor; Transmembrane.  
FT TOPO\_DOM 1 4 Cytoplasmic (Potential).  
FT TRANSMEM 5 27 Signal-anchor for type II membrane  
FT TOPO\_DOM 28 188 protein (Potential).  
FT DOMAIN 78 184 Extracellular (Potential).  
FT CARBOHYD 32 32 C-type lectin.  
FT CARBOHYD 93 93 N-linked (GLCNAC...) (Potential).  
FT CARBOHYD 144 144 N-linked (GLCNAC...) (Potential).  
FT CARBOHYD 151 151 N-linked (GLCNAC...) (Potential).  
FT DISULFID 71 82 By similarity.  
FT DISULFID 99 183 By similarity.  
FT DISULFID 161 175 By similarity.  
FT VARSPLIC 116 116 Missing (in isoform 2).  
FT MUTAGEN 16 16 K->I: Abolishes interaction with TYROBP.  
SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
Query Match 15.5%; Score 159; DB 1; Length 188;  
Best Local Similarity 26.5%; Pred. No. 5.8e-07;  
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;  
QY 41 ITLGLTAVLSV-----LLYQWILCOGSN-----YSTC-----ASCPS----- 74  
DB 6 IISGLIVLVKRVKMTLLFLYFPQIFNKSNDEGFTTTRSGYVSQIRGSSSPSPNGFITTR 65  
QY 75 -----CPDRMKYGNHCYFYSVEEKDMSLSLEFCIARDSHLVITDNOEMLQVFLSEA 129  
DB 66 SYGTVCPKMEFYQARCFPLSTSESSWNSRDFCKGKSTLAVNTPKLFQDITDAE 125  
QY 130 FCWIGL---RNSGMRWEDGSPINFRISNSFVOTCGAIN-KNGIQASSCEVPLHGVC 185  
DB 126 KYFICGLIYHREKRWKRNINSVFN-GNVTNQNQNFNCATIGLTKTPDAACDISYRICE 184  
QY 186 K 186  
DB 185 K 185  
RESULT 8  
Q52M11\_HUMAN PRELIMINARY; PRT; 188 AA.  
AC Q52M11; HUMAN  
DT 11-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 11-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE C-type lectin, superfamily member 5.  
GN Name=CLECTA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=lung and heart;  
RC MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Tohtiyuki S., Carninci P., Schaefer C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=lung and heart;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC093714; AAH93714.1; mRNA.  
KW Lectin.  
SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
Query Match 15.5%; Score 159; DB 2; Length 188;  
Best Local Similarity 26.5%; Pred. No. 5.8e-07;  
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;  
QY 41 ITLGLTAVLSV-----LLYQWILCOGSN-----YSTC-----ASCPS----- 74  
DB 6 IISGLIVLVKRVKMTLLFLYFPQIFNKSNDEGFTTTRSGYVSQIRGSSSPSPNGFITTR 65  
QY 75 -----CPDRMKYGNHCYFYSVEEKDMSLSLEFCIARDSHLVITDNOEMLQVFLSEA 129  
DB 66 SYGTVCPKMEFYQARCFPLSTSESSWNSRDFCKGKSTLAVNTPKLFQDITDAE 125  
QY 130 FCWIGL---RNSGMRWEDGSPINFRISNSFVOTCGAIN-KNGIQASSCEVPLHGVC 185  
DB 126 KYFICGLIYHREKRWKRNINSVFN-GNVTNQNQNFNCATIGLTKTPDAACDISYRICE 184  
QY 186 K 186  
DB 185 K 185  
RESULT 9  
Q8C634\_MOUSE PRELIMINARY; PRT; 189 AA.  
AC Q8C634; MOUSE  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 30, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:4922502D1 product:hypothetical C-type lectin domain  
DE containing protein, full insert sequence (Similar to C lectin-related  
DE protein A).  
GN Name=4922502D21Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Testis;  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.,  
RT "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arai T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Pleischmann W., Gaasterland T., Giesi C., King B., Koochi H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Oxford J., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher M., Fujita A., Gariboldi M.,  
 RA Guernicchi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Oosato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gyojibori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kani A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lennarz B., Lyons P.A.,  
 RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempke C.A., Seton M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Wanabue Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shitaki T., Waki K., Kawai I., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Hatada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watanabe M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [6]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,  
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Katsunai T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsumoto H., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshitsugu S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smalls D.E.,  
 RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Testis;  
 RA Director MGC Project;  
 RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK076635; BAC6425.1; -; mRNA.  
 DR EMBL; BC089479; AAH89479.1; -; mRNA.  
 DR EMBL; ENSMUSG0000047720; Mus musculus.  
 DR MGI; MGI:2685920; 4922502D21Rik.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C\_1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS50041; C TYPE LECTIN\_2; 1.  
 KW Hypothetical protein, lectin.  
 SQ SEQUENCE 189 AA; 22107 MW; 2EE5673DBACB239E CRC64;  
 Query Match 12.9%; Score 131.5; DB 2; Length 189;  
 Best Local Similarity 24.2%; Pred. NO.0.00024;  
 Matches 45; Conservative 34; Mismatches 86; Indels 21; Gaps 8;  
 QY 19 QNDYGPQKSSSSKPSGSCIV-----AITGLITRAVLISLTY-----OMILQGSNY 66  
 DB 2 QDTPSPRLPQSHRRHRLMFDAKAVLTLLTLLGAAVAVALWGFSPPRKRTVTRARN 61  
 QY 67 STC-ASCSPCDRWKYNHCYFSEVERKDNSSLEFLARDSHLYVTTDNGEMSLQVF 125  
 DB 62 KTCDDVEVLCPEDWVKLRQNCPSRIQHNKSWLTANDTELDATVATVITDKTEVILMNQ 121  
 QY 126 LSE-AFCWIGL--RNNSG-WRMEDGSPL-NFSRISNSNFVOTCGAINKNGIQASSCEVPL 180  
 DB 122 IOEMKTYIIGLRQGLGIWWTNOSKYNLHEIQDH---QCAVHQKIGDSTSCEDPX 178  
 QY 181 HGVCCK 186  
 :|:



RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durlin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Gloeck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laebo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Modyarty C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Muskern D.R., Pacleby J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Palerit K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Sider-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhou X., Zhu S., Zhu X., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE:22426065; PubMed:12537568;  
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleby J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE:22426070; PubMed:12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celinker S.E.,  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomic perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE:22426069; PubMed:12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettecourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.,  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RX Berkeley *Drosophila* Genome Project;  
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleby J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.,  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RX Flybase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
[7]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Berkeley;  
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleby J.,  
RA Park S., Wan K., Yu C., Rubin G.M., Celinker S.,  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003471; AAF47464.1; -; Genomic\_DNA.  
DR EMBL; BT012477; AAS93748.1; -; mRNA.  
DR HSSP; P08661; 1B74.  
DR Ensembl; CG9134; *Drosophila melanogaster*.  
DR Flybase; FBgn003199; CG9134.  
DR GO; GO:0005528; F:sugar binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C.1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C TYPE LECTIN\_1; UNKOWN\_1.  
DR PROSITE; PS00411; C TYPE LECTIN\_2; 1.  
SQ SEQUENCE 189 AA; 21848 MW; 51E6C22082CD39DE CRC64;

Query Match 10.1%; Score 103.5; DB 2; Length 188;  
Best Local Similarity 21.0%; Pred. No. 0.11;  
Matches 39; Conservative 26; Mismatches 66; Indels 55; Gaps 9;

QY 49 VLSTLYLQWMLC-----QGSNSTCASCPC-----PDRW-----MKYGNHCYF 89  
DB 5 LILSVIISLQQLCLDRMTATPPKGPVADCPNCVDSQYTPNKWMPPLKLGSKRYLL 64  
QY 90 SVEEK-DVNSSLFCLARDSHLVITDQEMSLQVFLSEAFWCIGLRNNGM----- 141  
DB 65 GIFFKAMFKATQYCRHYGMHLASISSQENDRLKLRD-----FGLGHEHFWISGTDLA 120  
QY 142 -----RWEDGSPINFRISNSFVQTCAL-NKNG-----LQASSCEVP 179  
DB 121 DEGNFWMATGRPIFTTMNAGEPNFR--YENGHEENCLEIMRNDGKGLKWNDSPPCFE 178  
QY 180 LHVYCK 185  
DB 179 TVFVCE 184

RESULT 13  
Q60SU3 CABR PRELIMINARY; PRT; 189 AA.  
ID Q60SU3;  
AC Q60SU3;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Hypothetical protein CBG20753 (Fragment).  
GN Name=CBG20753;  
OS Caenorhabditis briggsae.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxId=6238;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RG The C.briggsae Sequencing Consortium;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; CAAC01000115; CAE73324.1; -; Genomic\_DNA.  
DR GO; GO:0005528; F:sugar binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C.1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00411; C TYPE LECTIN\_2; 1.  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 189  
SQ SEQUENCE 189 AA; 21805 MW; 48F6021C793C4845 CRC64;

Query Match 9.4%; Score 96.5; DB 2; Length 189;  
Best Local Similarity 22.6%; Pred. No. 0.53;  
Matches 42; Conservative 33; Mismatches 70; Indels 41; Gaps 10;



This page blank (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OW protein - protein search, using SW model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3962 Seconds  
(without alignments)  
988,409 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023  
Sequence: 1 MTDVSIVYSMLELPATQAQN.....GLQASSCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	2 I59421	mast cell function
2	92.5	9.0	188	2 T33623	hypothetical prote
3	55.5	5.7	188	2 F69262	hypothetical prote
4	55.5	5.4	189	2 T27306	hypothetical prote
5	55.5	5.4	188	2 A39185	hypothetical prote
6	55.5	5.4	189	2 T19559	hypothetical prote
7	54.5	5.3	189	1 ERAD75	early E3 20.6K gly
8	54.5	5.3	189	2 D82719	tryptophan repress
9	52.5	5.1	189	1 JCS394	Dz-1 protein - hum
10	49.5	4.8	189	1 ERAD35	early E3 20.5K gly
11	49.5	4.8	189	2 S52803	hypothetical prote
12	49.5	4.8	189	2 AE1446	probable scaffold
13	48.5	4.7	189	2 AH3634	more protein [impo
14	48.5	4.7	188	2 AC1355	methyldiaphosphor
15	48.5	4.7	188	2 H80106	60S ribosomal prot
16	48.5	4.7	189	2 AG1947	hypothetical prote
17	47.5	4.6	189	2 S78046	ribonuclease 6 (EC
18	47.5	4.6	189	1 IYHUF	interferon alpha-1
19	47.5	4.6	189	2 I84464	interferon-alpha-F
20	47.5	4.6	189	2 AD3015	conserved hypotet
21	47.5	4.6	189	2 C98269	probable general s
22	46.5	4.5	188	2 JCS347	high sulfur protei
23	46.5	4.5	188	2 DB1564	hypothetical prote
24	45.5	4.4	188	2 G75326	probable 16S rRNA
25	44.5	4.3	189	2 S34632	dnab protein hmo1
26	44.5	4.3	188	2 T17574	hypothetical prote
27	44.5	4.3	189	2 A25556	hypothetical 21.2K
28	44.5	4.3	189	2 A86369	hypothetical prote
29	43.5	4.3	188	1 DDBPC2	dCMP deaminase (EC

30	43.5	4.3	188	2 S77089	hypothetical prote
31	43.5	4.3	188	2 D84468	hypothetical prote
32	43.5	4.3	189	2 S48914	hypothetical prote
33	43.5	4.2	189	2 E86707	transcription regu
34	43.5	4.2	189	2 JX0235	core protein MGC-2
35	42.5	4.2	188	2 S67051	hypothetical prote
36	42.5	4.2	188	2 AH2548	hypothetical prote
37	42.5	4.2	189	2 G90855	hypothetical prote
38	42.5	4.2	189	2 E69410	acetoin utilization
39	42.5	4.1	188	2 AB0878	probable membrane
40	42.5	4.1	188	2 S09789	hypothetical prote
41	42.5	4.1	188	2 S41600	adrenomedullin - p
42	42.5	4.1	188	2 T46272	hypothetical prote
43	42.5	4.1	189	1 C1W01	insecticynin - to
44	42.5	4.1	189	2 AB0361	probable iron-sulp
45	41.5	4.1	188	2 B82183	ankk protein VC158

## ALIGNMENTS

RESULT 1  
159421  
mast cell function associated antigen - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I59421  
R/Guthmann, M.D.; Tal, M.; Pecht, I.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995  
A/Title: A secretion inhibitory signal transduction molecule on mast cells is another C  
A/Reference number: I59421, PMID:96016176; PMID:7568140  
A/Accession: I59421  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-188 <RES>  
A/Cross-references: UNIPROT:Q64335; UNIPARC:UPI000030101; EMBL:X79812; NID:G1020141; P  
A/Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; length 188;  
Best local Similarity 53.5%; Pred. No. 5.5e-42;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY	1	MTDVSIVYSMLELPATQAQNDYGPQOKSSSKSCGCVATITGLTAVLSTLVYQWIL	60
DB	1	MADNSIVSTLELPAPRVDDSRMKVAVLHRCVSYLVNVALGLTVILMSLLYQRTL	60
QY	61	COGSNVTGASCPSPDMKYGNNHCYFSEKEDMNSLIEFCLARDSHLVITDQEMS	120
DB	61	CCSGKGFMCQCRCRPLVMKRNASHCYFEMEKRDNNSSLKFCADKSHLLTFPDQGVN	120
QY	121	ILQVPLSEAFPCWIGLRNNSGWRWEDGSPILNFSRISSNFVQTCGAINKGLQASSCEVPL	180
DB	121	LPQEVGEDFYWIGLRIDDMRWEDGPAISLS-ILSNSVYQKGTTHRCGLHASSCEVAL	179
QY	181	HGVCKKV 187	
DB	180	QWICEKV 186	

RESULT 2  
T33623  
hypothetical protein F40G9.10 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T33623  
R/Gaves, T.; Sutereer, C.; Ozersky, P.  
Submitted to the EMBL Data Library, October 1998  
A/Description: The sequence of C. elegans cosmid F40G9.  
A/Reference number: Z21378  
A/Accession: T33623  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA

A:Residues: 1-188 <GRA>  
 A:Cross-references: UNIPROT:O9TZ75; UNIPARC:UPI000007BD20; EMBL:AF099919; PIDD:AC68804.  
 A:Experimental source: strain Bristol N2; clone F40G9  
 C:Genetics:  
 A:Gene: CESP:F40G9.10  
 A:Map position: 3  
 A:introns: 63/3; 99/1; 113/3; 153/3

Query Match 9.0%; Score 92.5; DB 2; Length 188;  
 Best Local Similarity 31.4%; Pred. No. 0.23;  
 Matches 27; Conservative 10; Mismatches 32; Indels 17; Gaps 4;

Qy 79 WKYGNHCYFVSVEKDNSSLEFCLARDSHLLVI---TDNOMSLQVFLSEA----- 129  
 Db 54 WESYTNFCYKSTAPARAFDANACRSESELSHSLTENQFL----VQLSAAGNRVNS 109

Qy 130 ---FCWIGL-RNNSGWRMEDSGPLNF 151  
 Db 110 KTNVYVIGLIFENRREWSMTDGSVVNY 135

RESULT 3  
 F69262  
 hypothetical protein AF0102 - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: F69262  
 R:Kleink, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 ; Goddek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Uteback, T.; Cottom, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Moose, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-188 <KLE>  
 A:Cross-references: UNIPROT:O30134; UNIPARC:UPI000005722A; GB:AE001099; GB:AE000782; NID

Query Match 5.7%; Score 58; DB 2; Length 188;  
 Best Local Similarity 34.5%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 4; Mismatches 16; Indels 18; Gaps 2;

Qy 118 EMSLLQVF-----LSEAFWIGLRNNSGWRMEDSGPLNSRISNSFVOTCAINKG 170  
 Db 14 KMRLLKLMKMDLSRISCEIGLRKQ-----SLPHKFLNTFGLIERNG 58

RESULT 4  
 T27306  
 hypothetical protein Y68A4B.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T27306  
 R:Matthews, L.  
 submitted to the EMBL Data Library, June 1998  
 A:Reference number: Z20341  
 A:Accession: T27306  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-189 <WIL>  
 A:Cross-references: UNIPROT:Q9XNR7; UNIPARC:UPI0000080A07; EMBL:AL023851; PIDD:CAA19555.  
 A:Experimental source: clone Y68A4B  
 C:Genetics:  
 A:Gene: CESP:Y68A4B.2  
 A:Map position: 5  
 A:introns: 21/1; 41/3; 78/1

Query Match 5.4%; Score 55.5; DB 2; Length 189;  
 Best Local Similarity 19.8%; Pred. No. 6.7e+02;  
 Matches 25; Conservative 14; Mismatches 42; Indels 45; Gaps 5;

Qy 75 CPDRMK-----YGNHCY-----FVSEKDNSSLEFCLARDSHLLVTDNOMSLQVF 125  
 Db 23 CPTGAGQDERPSPGFWICAKFRDGIOTYDAQA---CGAGAYLSGIQNVENQMMAGL 79  
 Qy 126 LSEAFWIGLRNNS-----GWRMEDSGPLNSRIS 155  
 Db 80 AMTGCHWLGARTRACIGQLVATCTRLNSFEWTDGATGDFWRLSDGPPNN---LF 136  
 Qy 156 SNSFVQ 161  
 Db 137 LNVFIQ 142

RESULT 5  
 A39185  
 virulence protein pagC precursor - Salmonella typhimurium  
 C:Species: Salmonella typhimurium  
 C:Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 09-Jul-2004  
 C:Accession: A39185  
 R:Pulkkinen, W.S.; Miller, S.I.  
 J. Bacteriol. 173, 86-93, 1991  
 A:Title: A Salmonella typhimurium virulence protein is similar to a Yersinia enterocolit  
 A:Reference number: A39185; MUID:91100323; PMID:1846140  
 A:Accession: A39185  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-188 <PU>  
 A:Cross-references: UNIPROT:P23988; UNIPARC:UPI000014786E; GB:M55546; NID:G154232; PIDD:  
 C:Superfamily: phage lambda membrane protein Iom

Query Match 5.4%; Score 55; DB 2; Length 188;  
 Best Local Similarity 36.8%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 9; Mismatches 9; Indels 6; Gaps 2;

Qy 138 NSGWRMEDSGPLNSRISNSFV---QTCAINKGL 171  
 Db 50 NVKRYEDDSPVSF--ISLSYLVGDRQAGSVEPEGI 85

RESULT 6  
 T19559  
 hypothetical protein C29F3.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T19559  
 R:Matthews, L.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19142  
 A:Accession: T19559  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-189 <WIL>  
 A:Cross-references: UNIPROT:O17613; UNIPARC:UPI00000783D6; EMBL:Z81043; PIDD:CAB02800.1;  
 A:Experimental source: clone C29F3  
 C:Genetics:  
 A:Gene: CESP:C29F3.4  
 A:Map position: 5  
 A:introns: 32/3; 133/3

Query Match 5.4%; Score 55; DB 2; Length 189;  
 Best Local Similarity 29.7%; Pred. No. 7.5e+02;  
 Matches 11; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 73 PSCPRMKY-----GNHCYFVSVEKDNSSLEFCLA 105  
 Db 33 PVPFAGWFOFORATGMLCYIPATPGAGWTTPOAACOA 69

RESULT 7  
 ERA075  
 early E3 20.6K glycoprotein - human adenovirus 7 (strain Gomen)  
 C:Species: Mastadenovirus h7 (human adenovirus 7)

A:Note: host Homo sapiens (man)  
 C:Date: 31-Mar-1990 #sequence\_rev:190 #text\_change 07-Nov-1997  
 C:Accession: A31830  
 R:Hong, J.S.; Mullis, K.G.; Engler, J.A.  
 Virology 167, 545-553, 1988  
 A:Title: Characterization of the early region 3 and fiber genes of Ad7.  
 A:Reference number: A94386; MUID:89073758; PMID:2849239  
 A:Accession: A31830  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HON>  
 A:Cross-references: UNIPARC:UPI0000174983; GB:M23666; NID:g341012  
 A:Note: the Genbank entry AD847FIBER PID:g576456 differs from the published sequence in C:Keywords: early protein; glycoprotein  
 F:73,137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.3%; Score 54.5; DB 1; Length 189;  
 Best Local Similarity 23.5%; Pred. No. 8.3e+02;  
 Matches 20; Conservative 19; Mismatches 13; Indels 33; Gaps 5;

Oy 3 DSVIYSMELPRTQAOXNGYPOO---KSSSSKPS---GSCVAI----- 41  
 Db 89 DSDVDNIIVPATTSA-----PRKTPSSSSAKASTIPKTSAMKDKIALNSTAPK 143  
 Oy 42 -----TLGLTLLAVLTYQWIKC 61  
 Db 144 TLPKSTIGITAVVGLIIT-FLC 166

RESULT 8  
 D82719  
 tryptophan repressor binding protein Xfl133 [imported] - Xylella fastidiosa (strain 9a5c  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_rev:190 #text\_change 09-Jul-2004  
 C:Accession: D82719  
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82815; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: D82719  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-189 <SIM>  
 A:Cross-references: UNIPROT:Q9PE95; UNIPARC:UPI00000C2626; GB:AE003949; GB:AE003849; NID  
 A:Experimental source: strain 9a5c  
 R:Simson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 Bionnes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
 aa-Neto, E.; Docena, C.; El-Dorty, H.; Facincant, A.P.; Ferreira, A.J.S.  
 submitted to Genbank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 Chado, M.A.; Madeira, A.M.F.; Kempner, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Marques, M.V.; Martins, E.  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.;  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
 M.; Tsuchino, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: Xfl133  
 C:Superfamily: flavodoxin

Query Match 5.3%; Score 54.5; DB 2; Length 189;  
 Best Local Similarity 28.1%; Pred. No. 8.3e+02;  
 Matches 18; Conservative 8; Mismatches 29; Indels 9; Gaps 1;

Oy 116 NOEWSLLQVFLSEAFPCWIGLRNNSGWRWEDGSPILNFSRISSNSFVOTCGAINKNGQASS 175  
 Db 106 NSLMSVTLFAAQHGIWVGDLMPGNSSSTGSPNDINRLGWSLGVMT-----QANN 156  
 Oy 176 CEVP 179

```

Db      157 DEAP 160

RESULT 9
JC5394
Df-1 protein - human
C:Species: Homo sapiens (man)
C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
JAccession: JC5394
R:Nakagudo, D.; Taira, T.; Kikura, H.; Ikeda, M.; Tamai, K.; Iguchi-Arigo, S.M.M.; Arii,
Biotech. Biophys. Res. Commun. 231, 509-513, 1997
A>Title: Df-1, a novel oncogene which transforms mouse NIH3T3 cells in cooperation with
A:Reference number: JC5394; PMID:97223489; PMID:9070310
A:Accession: JC5394
A:Molecule type: mRNA
A:Residues: 1-189 <NG>
A:Cross-references: UNIPROT:Q99497; UNIPARC:UPI0000072609; DBBJ:D61380; NID:G914937; PIR:
C:Comment: This protein is involved in a Ras-related signal transduction pathway.
C:Genetics:
A:Gene: GDB:DJ1
A:Cross-references: GDB:175839; OMIM:602533

Query Match          5.1%; Score 52; DB 1; Length 189;
Best Local Similarity 31.9%; Pred. No. 1.4e+03;
Matches 23; Conservative 9; Mismatches 26; Indels 14; Gaps 4;

QY      44 GLTRAVLL--SVLLYWILCOGSNYSFSCASCPCSPDRMKYGNHCFYFSVEKDM----- 96
           |||::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      100 GLIAITCGPTALLAHETGC-GSKVTT---HPLAKDKRMNGHTYSENRYEKDGLILTS 155
           :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY      97 ---NSLLEFCIA 105
           :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      156 RGPGRSFEFFALA 167

RESULT 10
BRAD35
early E3 20.5K glycoprotein - human adenovirus 3
C:Species: Mastadenovirus h3 (human adenovirus 3)
C:date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
JAccession: F29500
R:Signaes, C.; Akusjaervi, G.; Petersson, U.
Gene 50, 173-184, 1986
A>Title: Region E3 of human adenoviruses; differences between the oncogenic adenovirus-
A:Reference number: A91566; MUID:87219876; PMID:3582978
A:Accession: F29500
A:Molecule type: DNA
A:Residues: 1-189 <SIG>
A:Cross-references: UNIPROT:P11322; UNIPARC:UPI0000129ADF; GB:M15952; NID:G209901; PIDN
A>Note: The authors translated the codon ATG for residue 161 as Ile and TTG for 165 as
C:Superfamily: adenovirus early E3 20.5K glycoprotein
C:Keywords: early protein; Glycoprotein
F.73.137/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match          4.8%; Score 49.5; DB 1; Length 189;
Best Local Similarity 22.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 20; Mismatches 13; Indels 33; Gaps 5;

QY      3 DSVIYSMELPRTATQANDYGPQ---KSSSKPS-----CSCLVAI----- 41
           :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      89 NSLDVDNIIVVPATSA-----PRKSTFSSSSAKASTIPKTASAMDKLPKIALSNSTAAPN 143
           :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY      42 -----TLGLTAVLLSVLLYWILLC 61
           :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      144 TIPKSTIGITTAVVGLMI--FLC 166

RESULT 11
SS2803
hypothetical protein, 20.5K - human adenovirus 7
C:Species: Mastadenovirus h7 (human adenovirus 7)
C:date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
```

```
C:\Accession: S52803  
R:\Kajon, A.S.; Wadell, G.  
Submitted to the EMBL Data Library, April 1995  
A:\Description: Sequence analysis of the E3 region and fiber gene of human adenovirus 7h.  
A:\Reference number: S52798  
A:\Accession: S52803  
A:\Molecule type: DNA  
A:\Residues: 1-189 <KAL>  
A:\Cross-references: UNIPROT:Q83119; UNIPARC:UPI00000F8076; EMBL:Z48954; NID:G762955; PMID:  
A:\Experimental source: strain 87-922  
C:\Superfamily: adenovirus early E3 20.5K glycoprotein
```

Query Match 4.8%; Score 49.5; DB 2; Length 189;  
Best Local Similarity 22.4%; Pred. No. 2.4e+03;  
Matches 19; Conservative 20; Mismatches 13; Indels 33; Gaps 5;

OY 3 DSVIYSMELPLTAQAONDYGPOQ---KSSSKPS-----CSCVAI----- 41  
DB 89 NSLDNIIIVPATISA-----PRKSTPSSSAKASTIRKASAILKLKPITALSNSTAPN 143

OY 42 -----TLGLTAVLLSVLLYQMILC 61  
DB 144 TIKSTIGITRVVVGMILT--FLC 166

RESULT 12  
A:\1446  
probable scaffolding protein (Bacteriophage A118) lin0108 [imported] - Listeria innocua  
C:\Species: Listeria innocua  
C:\Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:\Accession: AB11446  
R:\Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocker,  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusserre, O.; Entian, K.D.; Fehl, H.  
Science 294, 849-852, 2001  
D.; Jones, L.M.; Karst, U.  
A:\Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maicourram, A.; Ma  
A:\Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maicourram, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,  
A:\Title: Comparative genomics of Listeria species.  
A:\Reference number: AB1077; MUID:21537279; PMID:11679669  
A:\Accession: AB11446  
A:\Status: preliminary  
A:\Molecule type: DNA  
A:\Residues: 1-189 <GLA>  
A:\Cross-references: UNIPROT:Q92PJ6; UNIPARC:UPI00000CC10B; GB:AUS92022; PIDN:CAC95341.1;  
A:\Experimental source: strain Clip11262  
C:\Genetics:  
A:\Gene: lin0108

Query Match 4.8%; Score 49.5; DB 2; Length 189;  
Best Local Similarity 23.7%; Pred. No. 2.4e+03;  
Matches 18; Conservative 13; Mismatches 24; Indels 21; Gaps 3;

OY 87 YFFSVEEDKNNSLEFCAR-----DSHLVTID-----NQMSILOVPLS 127  
DB 86 YQSEIAETKKKSATIELLASAKAKPKAVRALNDKLETDEGLKGLEDLEALQE--S 143

OY 128 EAFCWIGLRNNSGWRM 143  
DB 144 DAYLFAOESGSALKW 159

RESULT 13  
A:\H3634  
more protein [imported] - Brucella melitensis (strain 16M)  
C:\Species: Brucella melitensis  
C:\Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:\Accession: AH3634  
R:\DeVecchio, V.G.; Kaparat, V.; Redkar, R.D.; Patra, G.; Mujar, C.; Los, T.; Ivanova,  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:\Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:\Reference number: AJ3352; PMID:11756688  
A:\Accession: AH3634

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-189 <KUR>  
A:Cross-references: UNIPROT:O8YB99; UNIPARC:UPI00000566D6; GB:AE008918; PIDN:AAL54243.1;  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI11001  
A:Map position: II

Query Match                      4.7%; Score 48.5; DB 2; Length 189;  
Best Local Similarity 24.6%; Pred. No. 3e+03;  
Matches 16; Conservative 13; Mismatches 19; Indels 17; Gaps 4;

OY        92 EKD-----WNSLSEFCCLARDSHLV-ITDNOEMSLQVPLSEAFCIGLRNN---- 138  
         |||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB        19 EEEDLLMLVLWVSELITPAILLDAFMVMSVVDPOGVGLRAHLSPG---LAATNTVILL 75

OY        139 -SGWR 142  
         |||:  
DB        76 MSGWQ 80

RESULT 14  
AC1355  
methylinphosphotriester-DNA alylitransferase and transcription regulator homolog lmo2243 [  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AC1355  
R:Glaser, P.; Rangelul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker  
., Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusenget, O.; Entian, K.D.; Feihl, H.  
D.; Jones, U.W.; Karst, U.  
Science 294, 849-852, 2001  
A:Author: Kreft, J.; Kuhn, M.; Kunst, F.; Kutzkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
A>Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1355  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-188 <GLA>  
A:Cross-references: UNIPROT:O8Y533; UNIPARC:UPI000000C1EE; GB:NC\_003210; PIDN:CAD00321.1  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo2243  
C:Superfamily: methylinphosphotriester-DNA methyltransferase; methylinphosphotriester-DNA me

Query Match                      4.7%; Score 48; DB 2; Length 188;  
Best Local Similarity 26.2%; Pred. No. 3.3e+03;  
Matches 17; Conservative 12; Mismatches 34; Indels 2; Gaps 2;

OY        67 STCASC-PSCPDPMWKYGNGHCYFVSVEEKDMNSLSEFCCLARDSHLVITDNOEMSLQVF 125  
         |||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB        31 STFICYSCKSRRLRKKNIVIFHSAEA-FSHGYACKCKCKGGGSLPDTIEWNNIEMY 89

OY        126 LSEAF 130  
         : | : | :  
DB        90 IKENF 94

RESULT 15  
H90106  
60S ribosomal protein L9 [imported] - Giardia theta nucleomorph  
C:Species: nucleomorph Giardia theta  
A>Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H90106  
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei  
Nature 410, 1091-1096, 2001  
A>Title: The highly reduced genome of an enslaved algal nucleus.  
A:Reference number: A99082; MUID:11323671; PMID:11323671  
A:Accession: H90106  
A:Status: preliminary  
A:Molecule type: DNA



100 Books (USPO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 14:41:26 ; Search time 87.515 Seconds  
(without alignments)  
943.913 Million cell updates/sec

Title: US-09-811-367b-5

Sequence: 1 MADNSIYSTLELPAAPRVOD.....GLHSSCEVALQWICKVLP 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 6014

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	AAR77033 Mammalian
2	1036	100.0	188	2	AAW88277 Rat mast
3	1036	100.0	188	4	AAE11761 Rat mast
4	838	80.9	188	4	AAE11760 Mouse mas
5	545.5	52.7	189	7	ADD25635 Binding d
6	545.5	52.7	189	9	ADY19892 PRO polyp
7	525.5	50.7	189	2	AAW88265 Human mas
8	525.5	50.7	189	4	AAE11759 Human mas
9	154.5	15.9	188	4	AAE89021 Chicken M
10	159.5	15.4	188	4	AAW78675 Human pro
11	159.5	15.4	188	4	AAU06771 Human INT
12	159.5	15.4	188	6	ABO32533 Secreted
13	159.5	15.4	188	7	ADP65310 Human c-t
14	159.5	15.4	188	8	ADQ10144 Human pol
15	159.5	15.4	188	8	ADP25141 PRO polyp
16	153.5	14.8	189	4	AAU19837 Human nov
17	153.5	14.8	189	4	ABBI17910 Human ner
18	153.5	14.8	189	5	ABP48057 Human pol
19	153.5	14.8	189	7	ADCI1019 Human pro
20	92.5	8.9	189	4	ABBS9566 Drosophila
21	80.5	7.8	189	9	ABE70262 E-selectin
22	75.5	7.3	188	4	ABBS8823 Drosophila
23	75.5	7.3	189	7	ADC38690 Human sec
24	60	5.8	188	3	AAE60348 Arabidops

25	60	5.8	188	3	AAG19860 Arabidops
26	60	5.8	188	4	AAM39399 Human pol
27	59.5	5.7	188	8	ADN22989 Bacterial
28	56	5.4	188	3	AAE23544 Cytokine
29	56	5.4	189	5	ABBA7756 Listeria
30	55.5	5.4	189	6	ABU01363 S. pneumo
31	55	5.3	189	6	ABU11464 Human MDP
32	55	5.3	189	8	ADK68097 Plant ful
33	54	5.2	189	3	AAI19506 Arabidops
34	53.5	5.2	188	5	ABG70315 Human MDP
35	53.5	5.2	188	2	AAI35751 Chlamydia
36	53.5	5.2	189	4	AAE65153 Basic fib
37	52.5	5.1	188	8	ADK74859 Plant ful
38	52	5.0	188	5	ABBA48274 Listeria
39	52	5.0	188	8	ADT48905 Orl-assoc
40	50.5	4.9	188	3	AAE6736 Arabidops
41	50.5	4.9	188	4	AAU23356 Novel hum
42	50	4.8	188	3	AAU07314 Arabidops
43	50	4.8	188	8	ADK88330 Plant ful
44	48.5	4.7	189	1	AAI30179 Sequence
45	48.5	4.7	189	1	AAI40123 Sequence

#### ALIGNMENTS

RESULT 1  
AAR77033  
ID / AAR77033 standard; protein; 188 AA.

XX AAR77033;  
AC  
XX  
DT 01-FEB-1996 (first entry)  
XX  
XX Mammalian mast cell function-associated antigen (MAFA).  
DE  
XX  
XX Mast cell function-associated antigen; MAFA; soluble; ligand;  
KW identification; screening; inflammation; inflammatory; allergy; allergic;  
KW prevention.  
XX  
XX  
XX Rattus rattus.  
OS  
XX  
PN W09527734-A1.  
XX  
PD 19-OCT-1995.  
XX  
XX  
PF 06-APR-1995; 95MO-US004258.  
XX  
PR 08-APR-1994; 94IL-00109257.  
XX  
XX  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA (RYCU/) RYCUS A.  
XX  
XX  
PI Pecht I, Gutmann MD, Tal M;  
XX  
XX WPI, 1995-366356/47.  
DR N-PSDB; AAT01471.  
XX  
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -  
PT useful for screening for ligands of MAFA which are useful for prevention  
PT of inflammatory and allergic reactions.  
XX  
XX Claim 12; Page 37; 54pp; English.  
PS  
XX  
CC A soluble form of mast cell function-associated antigen (MAFA) can be  
CC produced by recombinant techniques for use in the ligand- screening  
CC assay. The ligands that are identified may be used alone or in  
CC combination with the MAFA to prevent inflammatory and allergic reactions  
XX  
SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;  
Best Local Similarity 100.0%; Pred. No. 3e-96;

```
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTVILMSLLYQRTL 60
DB 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTVILMSLLYQRTL 60
QY 61 CCGSGKGFMCSCQRCPCNLMNRNGSHCYFSEKRDWNSLKFCDKXSHLLTFPNOGVN 120
DB 61 CCGSGKGFMCSCQRCPCNLMNRNGSHCYFSEKRDWNSLKFCDKXSHLLTFPNOGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLISNSVYQKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLISNSVYQKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLTP 188
DB 181 WICEKVLTP 188

RESULT 2
AAM88277
ID AAM88277 standard; protein; 188 AA.
XX
XX AAM88277;
AC
XX
DT 29-MAR-1999 (first entry)
XX
DE Rat mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; splice variant; rat;
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
FT Modified-site 82..84
FT /note="Asn is N-glycosylated"
FT Modified-site 97..99
FT /note="Asn is N-glycosylated"
XX
XX WO9854209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GB001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewlett EL, Lamere MBAC, Lamont A, Williams DH;
XX
XX WPI; 1999-059806/05.
XX
XX N-PSDB; AAV84222.
XX
XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.
XX
XX Disclosure; Fig 4; 44pp; English.
XX
XX This is the amino acid sequence of rat mast cell function-associated
XX antigen (MAFA), a type II membrane glycoprotein found on mast cells and
XX basophils. The invention relates to cloning of the human MAFA molecule
XX (see AAM88265) and to the discovery of splice variants (see AAM88266-67)
XX of human MAFA that are not found in rat. Polypeptides and synthetic
XX peptides (see AAM88258-64) based on human MAFA and human truncated MAFA,
XX and polynucleotides encoding them, can be used in methods for the
XX treatment of inflammatory and allergic diseases (e.g. rheumatoid
XX arthritis and asthma), and tumour growth
XX
XX Sequence 188 AA;
SQ
```

```
Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTVILMSLLYQRTL 60
DB 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTVILMSLLYQRTL 60
QY 61 CCGSGKGFMCSCQRCPCNLMNRNGSHCYFSEKRDWNSLKFCDKXSHLLTFPNOGVN 120
DB 61 CCGSGKGFMCSCQRCPCNLMNRNGSHCYFSEKRDWNSLKFCDKXSHLLTFPNOGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLISNSVYQKCGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLISNSVYQKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLTP 188
DB 181 WICEKVLTP 188

RESULT 3
AAE11761
ID AAE11761 standard; protein; 188 AA.
XX
XX AAE11761;
AC
XX
DT 18-DEC-2001 (first entry)
XX
DE Rat mast cell function associated antigen (MAFA) protein.
XX
XX Rat; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
XX Rattus norvegicus.
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Miyayama T;
XX
XX WPI; 2001-611482/70.
XX
XX N-PSDB; AAD18736.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
```



CC NK cell or a T-cell. The present sequence is rat MAFa protein  
 XX  
 SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 4; Length 188;  
 Best Local Similarity 100.0%; Pred. No. 3e-96;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSTYSTLELPAAAPRVDDSRMKVAVLHRCVSYLVWVALGLITVIMSLLYQRTL 60  
 DB 1 MADNSTYSTLELPAAAPRVDDSRMKVAVLHRCVSYLVWVALGLITVIMSLLYQRTL 60  
 QY 61 CCGSKGFMCSQSCRCPNLMWRNGSHCYFYSMEKRDWNSLKFCADKXSHLTFPDNOGVN 120  
 DB 61 CCGSKGFMCSQSCRCPNLMWRNGSHCYFYSMEKRDWNSLKFCADKXSHLTFPDNOGVN 120  
 QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLTSLNSVVOCKGTHRCGLHASSCEVALQ 180  
 DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLTSLNSVVOCKGTHRCGLHASSCEVALQ 180  
 QY 181 WICEKVL 188  
 DB 181 WICEKVL 188

## RESULT 4

AAE11760  
 ID AAE11760 standard; protein; 188 AA.

AAE11760;

18-DEC-2001 (first entry)

Mouse mast cell function associated antigen (MAFA) protein.

XX Mouse; pharmaceutical composition; mast cell function associated antigen;  
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
 KM immunosuppressive; cyclostatic.

XX Mus sp.

XX Key Location/Qualifiers  
 FH Domain 64..188  
 FT /note= "Extracellular domain"

XX W0200170805-A2.

XX 27-SEP-2001.

XX 16-MAR-2001; 2001WO-US008596.

XX 17-MAR-2000; 2000US-0190716P.

XX (GEMINI-) GEMINI SCI INC.

XX Takahashi N, Miyayama T;

XX WPI; 2001-611482/70.

XX N-PSDB; AAD18735.

XX Pharmaceutical composition for treating tumor by stimulating cytotoxic  
 PT activity of natural killer cell or T-cell, comprises an agent that binds  
 PT to mast cell function-associated antigen ligand on target cell.

XX Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising  
 CC an agent which specifically binds to a mast cell function associated  
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
 CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA  
 CC ligand and a pharmaceutically acceptable excipient. The invention is  
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA  
 CC binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX Sequence 188 AA;

Query Match 80.9%; Score 838; DB 4; Length 188;  
 Best Local Similarity 80.7%; Pred. No. 3.1e-76;  
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSTYSTLELPAAAPRVDDSRMKVAVLHRCVSYLVWVALGLITVIMSLLYQRTL 60  
 DB 1 MADNSTYSTLELPAAAPRVDDSRMKVAVLHRCVSYLVWVALGLITVIMSLLYQRTL 60  
 QY 61 CCGSKGFMCSQSCRCPNLMWRNGSHCYFYSMEKRDWNSLKFCADKXSHLTFPDNOGVN 120  
 DB 61 CCGSKGFMCSQSCRCPNLMWRNGSHCYFYSMEKRDWNSLKFCADKXSHLTFPDNOGVN 120  
 QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLTSLNSVVOCKGTHRCGLHASSCEVALQ 180  
 DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPALSLTSLNSVVOCKGTHRCGLHASSCEVALQ 180  
 QY 181 WICEKVL 187  
 DB 181 WICEKVL 187

## RESULT 5

ADD25635  
 ID ADD25635 standard; protein; 189 AA.

ADD25635;

15-JUN-2004 (first entry)

Binding domain-immunoglobulin fusion protein-associated protein #95.

XX Binding domain; immunoglobulin; fusion protein; cyclostatic;  
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
 KW neuroprotective; hinge region; immunoglobulin heavy chain;  
 KW CH2 constant region; CH3 constant region; IgG1;  
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

XX US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

XX 17-JUN-2002; 2002US-00053530.

XX 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENE-CRAFT INC.

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a  
 PT subject having or suspected of having a malignant condition or a B-cell  
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

CC The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 189 AA;

Query Match 52.7%; Score 545.5; DB 7; Length 189;

Best Local Similarity 55.1%, Pred. No. 1.1e-46;

Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIVSTLELPAAAPRVQDDSRMKVAVLHRCVSYLVMAALGLTVIMSLLYORTL 60  
DB 1 MTDVSIYSLMLPRTATQANDYGPQKSSSRPSCVLAIALGLTAVLSVLLYQWTL 60  
QY 61 CCGSKGFMCSCQSRCPNLMRNNGSHCYFSEKRDWNSLKFCAKGSHTLTPDNGVN 120  
DB 61 CCGSNVSTCASCPCSDRMWKGYNHCYFSEKDWNSLKFCLARDSHLLVITDNOEWS 120  
QY 121 LFGVYGDGFYWGIGRDIDGKRWEDGPAALSLTSLNSVVGKCGTHRCGLAASCEVAL 179  
DB 121 LLOVFLSEAFWIGIRLNNNGMRWEDGSPNLSFVQTCGAINKGLQASSCEVPL 180  
QY 180 QWICEKV 186  
DB 181 HMVCKKV 187

RESULT 6  
ADY19892  
ID ADY19892 standard; protein; 189 AA.

XX ADY19892;  
DT 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 5698.

DE Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
XX Antirheumatic; Anticholesteric; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Vitruicide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
XX Antiallergic; diagnosis.

OS Homo sapiens.

FN WO2005016962-A2.

PD 24-FEB-2005.

PP 11-AUG-2004; 2004WO-US026249.

PR 11-AUG-2003; 2003US-0493546P.

PA (GETH ) GENENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

DR WPI; 2005-182330/19.

PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 5698; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO  
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,  
XX composition, and method are useful for diagnosing and treating an immune  
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid  
XX arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 189 AA;

Query Match 52.7%; Score 545.5; DB 9; Length 189;

Best Local Similarity 55.1%, Pred. No. 1.1e-46;

Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIVSTLELPAAAPRVQDDSRMKVAVLHRCVSYLVMAALGLTVIMSLLYORTL 60  
DB 1 MTDVSIYSLMLPRTATQANDYGPQKSSSRPSCVLAIALGLTAVLSVLLYQWTL 60  
QY 61 CCGSKGFMCSCQSRCPNLMRNNGSHCYFSEKRDWNSLKFCAKGSHTLTPDNGVN 120  
DB 61 CCGSNVSTCASCPCSDRMWKGYNHCYFSEKDWNSLKFCLARDSHLLVITDNOEWS 120  
QY 121 LFGVYGDGFYWGIGRDIDGKRWEDGPAALSLTSLNSVVGKCGTHRCGLAASCEVAL 179  
DB 121 LLOVFLSEAFWIGIRLNNNGMRWEDGSPNLSFVQTCGAINKGLQASSCEVPL 180  
QY 180 QWICEKV 186  
DB 181 HMVCKKV 187

RESULT 7  
AAW88265  
ID AAW88265 standard; protein; 189 AA.

XX AAW88265;

DT 29-MAR-1999 (first entry)

DE Human mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA, splice variant; human;  
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

```
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 7..10
FT /note="ITIM motif"
FT Modified-site 65..67
FT /note="Asn is N-glycosylated"
FT Modified-site 97..99
FT /note="Asn is N-glycosylated"
FT Modified-site 137..139
FT /note="Asn is N-glycosylated"
FT Modified-site 150..152
FT /note="Asn is N-glycosylated"
XX
XX MO9854209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GB001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewlett EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX MPI; 1999-059806/05.
XX
XX N-PSDB; AAV84198.
XX
XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.
XX
XX Disclosure; Fig 1; 44pp; English.
XX
XX This is the amino acid sequence of human mast cell function-associated
XX antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
XX encoding human MAFA can be obtained from myelogenous leukaemic cell line
XX KU812 or cDNA derived from human lung tissue. The encoded protein is
XX similar to the rat form (see AMW88277) having an intracellular domain
XX containing a putative immunoreceptor tyrosine activation motif (ITIM) and
XX an extracellular lectin-like domain. 2 Alternatively spliced forms (see
XX AMW88266-67) of human MAFA have been identified. Polypeptides and
XX synthetic peptides (see AMW88258-64) based on these truncated MAFA
XX proteins can be used in methods for the treatment of inflammatory and
XX allergic diseases, and tumour growth
XX
XX Sequence 189 AA:
SQ
Query Match 50.7%; Score 525.5; DB 2; Length 189;
Best Local Similarity 53.5%; Pred. No. 1.2e-44;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
```

```
ID AAE11759 standard; protein; 189 AA.
XX
XX AAE11759;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human mast cell function associated antigen (MAFA) protein.
XX
XX Human; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
XX
XX MPI; 2001-611482/70.
XX
XX N-PSDB; AAD18734.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Claim 10; Page 18; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is human MAFA protein
XX
XX Sequence 189 AA:
SQ
Query Match 50.7%; Score 525.5; DB 4; Length 189;
Best Local Similarity 53.5%; Pred. No. 1.2e-44;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
```



QY	182	ICEX	185
	182	ICEX	185
DB	182	ICEX	185
RESULT 11			
ID	AAU00671	standard; protein; 188 AA.	
AC	AAU00671;		
XX	07-SEP-2001	(first entry)	
DE	Human INTERCEPT 289 form 1a polypeptide.		
XX	Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;		
KW	skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;		
KW	bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;		
KM	anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;		
KM	malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;		
KW	attention deficit disorder; Crohn's disease; gastroenteritis; goitre;		
KW	hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;		
XX	muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Domain	7. .27	
FT		/note= "Transmembrane domain"	
FT	Domain	28. .188	
FT		/note= "Extracellular domain"	
XX			
PN	WO200129088-A1.		
XX			
PD	26-APR-2001.		
XX			
PF	23-JUN-2000; 2000MC-US017386.		
XX			
PR	19-OCT-1999; 99US-00420707.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Mackay CR, Myers PS, KIRST SJ, Fraser CC, Leiby KR;		
XX			
PT	WPI; 2001-308477/32.		
XX			
DR	N-PSDB; AAS00661.		
XX			
PT	New isolated nucleic acid molecule for diagnosis, prevention, and therapy		
XX	of human and other animal disorder, or as modulating agent for regulating		
XX	cellular processes.		
XX			
XX	Claim 8; Fig 2A-2B; 263pp; English.		
XX			
CC	The sequence represents human INTERCEPT 289 form 1a polypeptide. This		
CC	protein and similar others exhibit the ability to affect growth,		
CC	proliferation, survival, differentiation, activity, morphology, or		
CC	movement/migration of, e.g. T cells and cells of the heart, liver,		
CC	pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph		
CC	node, peripheral blood leukocyte, bone marrow or thymus tissue. They can		
CC	be used as modulating agents for regulating cellular processes, thus, the		
CC	protein and their associated nucleic acids can be used to prognosticate,		
CC	prevent, diagnose, or treat disorders associated with physiological		
CC	processes. These disorders include abnormal blood coagulation, asthma,		
CC	anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery		
CC	disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,		
CC	meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,		
CC	goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary		
CC	embolism and muscular dystrophy. Antibodies to disorders such as these		
CC	can be made by providing a polypeptide of the invention to an immuno-		
CC	competent vertebrate and harvesting blood or serum from the vertebrate		
XX	Sequence 188 AA;		

Query Match	15.4%	Score 159.5	DB 4	Length 188
Best Local Similarity	25.5%	Pred. No. 1.1e-07		
Matches 47	Conservative 31	Mismatches 65	Indels 41	Gaps 7
QY	40	MVALGLTLVLV-----MSLL-----YQRTLCGCS-----KGFMC	70	
DB	5	MISGLIYVVLKVVGMITFLFLYFPIQFNKNDGFTTTSYGVQSIFGSSSPNGFI	64	
QY	71	QC--SRCENLMWRNGSHCYFSEMEKRDWNSLIFKFCAGSHLLTPDNQVNLFOEYVGE	128	
DB	65	RSYGVCPKDMEFQARCFPISTSSSNESDFFCKGKSTLAIYNTPEKLFLODITDA	124	
QY	129	DFYWIGL--RDIDGWRNEDGPALSLTSLNSVYKCGTIHRCGL---HASSCEVALQW	181	
DB	125	EKYFTGLIYHREEXKRWIINNSVFNGVNTNOMFNFCATI---GLTKTFDASCDISYR	181	
QY	182	ICEK 185		
DB	182	ICEK 185		
RESULT 12				
ABO32533	standard; protein, 188 AA.			
ID	ABO32533			
XX	ABO32533;			
XX	17-SEP-2003	(first entry)		
DE	Secreted polypeptide-related protein #18.			
XX	Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;			
KW	hormonal disorder; proliferative disorder; cancer; thyroid disorder;			
KW	diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;			
KW	Alzheimer's disease; Parkinson's disease; cardiovascular disorder;			
KW	myocardial infarction; congestive heart disease; blood platelet disorder;			
XX	thrombocytopenia; blood vessel; atherosclerosis; vasculitis.			
OS	Homo sapiens.			
XX	US2003022279-A1.			
PN	30-JAN-2003.			
PD	12-JAN-2001; 2001US-00759130.			
PF	14-JUN-1999; 99US-00333159.			
XX	29-JUN-1999; 99US-00342364.			
PR	10-SEP-1999; 99US-0039396.			
PR	19-OCT-1999; 99US-00480707.			
PR	07-JAN-2000; 2000US-00479249.			
PR	27-APR-2000; 2000US-00559497.			
PR	24-MAY-2000; 2000US-00578063.			
PR	16-JUN-2000; 2000US-00596194.			
PR	23-JUN-2000; 2000US-00602871.			
PR	30-JUN-2000; 2000US-00608452.			
XX	(FRAS/) FRASER C C.			
PA	(BARN/) BARNES T M.			
PA	(SHAR/) SHARP J D.			
PA	(KIRS/) KIRST S J.			
PA	(MYER/) MYERS P S.			
PA	(LEIB/) LEIBY K R.			
PA	(HOIT/) HOITZMAN D A.			
PA	(MCCA/) MCCARTHY S A.			
PA	(WRIG/) WRIGHTON N.			
PA	(MACK/) MACKAY C R.			
PA	(GOOD/) GOODEARL A D J.			
XX	Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;			
PI	Holtzman DA, Mccarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;			
XX	DOI: 10.1003-456290/43.			

DR N-PSDB; ACDD66719, ACDD66720.

PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202.  
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
PT treating disorders such as cancer, diabetes or atherosclerosis, and in  
PT forensic biology.

PS Claim 9; Fig 11A-11C; 482pp; English.

CC The invention relates to secreted polypeptide-related proteins and  
CC nucleic acids (TRANO and INTERCEPT proteins and nucleic acids). The  
CC nucleic acids, proteins and antibodies specific to the proteins are  
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and  
CC prophylactic and therapeutic methods. The sequences are used in  
CC diagnosing, preventing or treating proliferative disorders (e.g.  
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders  
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
CC disorders (e.g. myocardial infarction or congestive heart disease), blood  
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
CC acids may also be used in chromosome mapping, tissue typing and forensic  
CC biology, and as surrogate markers. This sequence represents a secreted  
CC polypeptide-related protein of the invention. Note: The sequence data for  
CC this patent was obtained in electronic format directly from USPTO at  
CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

**SQ Sequence 188 AA;**

Query Match	15.4%	Score 159.5;	DB 6;	Length 186;
Best Local Similarity	25.5%	Pred. No. 1.1e-07;		
Matches 47; Conservative	31;	Mismatches 65;	Indels 41;	Gaps 7

QY 40 MVALGLTLYL-----MSLL-----YQRLCCGS-----KGMCS 70  
 D 5 MIISGLIVLVKLVGMTLLFLYEPQLFNKSDNGFTTTSYGVQSLPSSSPNGIIT 64  
 QY 71 QC--SRCPNLMMNGSHCYTFSEMEKRDWNSLKFCADGSHLLTFPDNGVNLFOEYVE 128  
 D 65 RSYGVTCPPKMEFYQARCFPLSTSESMWESDFFCKGGSLTALVNPTEKFLQDITTD 124  
 QY 129 DPYWIGL---RDIDGRMEDGPAISLISNSVQCGTIRHCGL---HASSCEVALQW 161  
 D 125 EKFFIGILYHREKERRMRTINNSVFQNTVNNQNFENCAIT---GLTKFDASCDISYR 161

QY	182	ICEK	185
Db	182	ICEK	185

RESULT 13  
ADP65310  
ID ADP65310 standard; protein; 188 AA.

AC ADP653107

DT 12-AUG-2004 (first entry)

DE Human c-type (calcium dependent, carbohydrate-recognition domain) lectin.

KM autoimmune disease; arthritis; gene expression analysis;  
KM rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic  
KM antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;  
KM immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KM immune; human.

**Homo sapiens.**

PN WO2003072827-A1.

PD 04-SEP-2003.

XX 31-OCT-2002; 2002WO-US035433.  
PF

PR 31-OCT-2001; 2001US-0336220P.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PI Hirsch R, Thorton SL;

DR WPI; 2003-712740/67

XX

PT profiles and microarray technology, useful for diagnosing and tre

PS Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; diagnosis or analysis of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIPO.

**SQ Sequence 188 AA;**

Query Match	15.4%	Score 159.5	DB 7	Length 188
Best Local Similarity	25.5%	Pred. No. 1.1e-07		
Matches 47; Conservative	31;	Mismatches 65;	Indels 41;	Gaps 7

[illegible]

## RESULT 14

XX

AC ADQ10144;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human polypeptide #25.  
 XX  
 KW Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;  
 KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;  
 KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;  
 KW arteriosclerosis; hypertension; bacterial infection; psoriasis;  
 KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;  
 KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;  
 KW golter; infertility; endometriosis; muscular disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004121396-A1.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 19-DEC-2003; 2003US-00741790.  
 XX  
 PR 14-JUN-1999; 99US-00333159.  
 PR 29-JUN-1999; 99US-00342364.  
 PR 10-SEP-1999; 99US-00393966.  
 PR 19-OCT-1999; 99US-00420707.  
 PR 07-JAN-2000; 2000US-00479249.  
 PR 27-APR-2000; 2000US-00559497.  
 PR 24-MAY-2000; 2000US-00578063.  
 PR 16-JUN-2000; 2000US-00596194.  
 PR 23-JUN-2000; 2000US-00602871.  
 PR 30-JUN-2000; 2000US-00608452.  
 PR 12-JAN-2001; 2001US-00759130.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Frazer CC, Barneer TM, Sharp JD, Kizet SJ, Myers PS, Leiby KR,  
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl AD;  
 XX  
 DR WPI; 2004-479675/45.  
 XX  
 PT New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and  
 PT treating cancer, constipation, hemorrhoids, cystic fibrosis,  
 PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,  
 PT tuberculosis, malaria, golter, infertility.  
 XX  
 PS Claim 9; SEQ ID NO 83; 483bp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The invention also relates to a host cell containing a  
 CC polynucleotide of the invention, an antibody which selectively binds with  
 CC a polypeptide of the invention, a method of detecting the presence of a  
 CC polypeptide in a sample, a method of identifying a compound which binds  
 CC with a polypeptide, and a method of modulating the activity of a  
 CC polypeptide. The polynucleotides, polypeptides and compositions are  
 CC useful for diagnosing, preventing and/or treating cancer, obesity,  
 CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host  
 CC reactions, allergic reactions, cystic fibrosis, hypogonadism,  
 CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,  
 CC hypertension, bacterial infections, psoriasis, diabetes mellitus,  
 CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's  
 CC disease, AIDS, tuberculosis, viral infections, malaria, golter,  
 CC infertility, endometriosis, wounds and muscular disorders. This sequence  
 CC represents a human polypeptide of the invention. Note: The sequence data  
 CC for this patent did not form part of the printed specification but was  
 CC obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 188 AA;  
 XX  
 Query March 15.4%; Score 159.5; DB 8; Length 188;  
 Best Local Similarity 25.5%; Pred. No. 1.1e-07;  
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;

QY 40 MYALGLLVIL-----MSLL-----YQRTLCSS-----KGFMS 70  
 DB 5 MISELIVLVKVGMTFLFYFQIFKNSDGFTTTSYGVTSQIFGSSSPNGFIT 64  
 QY 71 QC--SRCPNLWMRNGSHCYFSMERKDMNSILKPCADKSHLLTPPDNGVNLFOEYVGE 128  
 DB 65 RSYGVCRKDMEFYARCFPLSTSSSWNESRDFCKGSGTLAIYNTPEKLFLODITDA 124  
 QY 129 DFYWIGL---RDIDGRWEDGPAISLISLNSVOKGTIRHCGL---HSSGEVALQW 181  
 DB 125 EKYFGLIYHREKRWIMNSVFNQVNTQNFNCATF---GLTKTFDASCDISYR 181  
 QY 182 ICEK 185  
 DB 182 ICEK 185  
 RESULT 15  
 ID ADP25141  
 ID ADP25141 standard; protein, 188 AA.  
 XX  
 AC ADP25141;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE PRO polypeptide SEQ ID NO:2319.  
 XX  
 KW PRO; antiinflammatory; antiarthritis; antirheumatic; immunosuppressive;  
 KW osteopathic; antidiabetic; dermatologic; antipsoriatic; antiallergic;  
 KW antistematic; hepatotropic; respiratory; gene therapy; immune system.  
 XX  
 OS unidentified.  
 XX  
 PN WO2004041170-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034312.  
 XX  
 PR 01-NOV-2002; 2002US-0423394P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 DR WPI; 2004-419628/39.  
 DR N-PADB; ADP25140.  
 XX  
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.  
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
 PT renal disease, or demyelinating diseases of the central or peripheral  
 PT nervous system.  
 XX  
 PS Claim 7; SEQ ID NO 2319; 2940bp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid and the PRO  
 CC polypeptide encoded by it. A protein of the invention has  
 CC antiinflammatory, antiarthritis, antirheumatic, immunosuppressive,  
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
 CC antistematic, hepatotropic, and respiratory activity. A polynucleotide  
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
 CC agonist, antagonist, or antibody that specifically binds to the  
 CC polypeptide is useful for treating an immune related disorder such as  
 CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary





GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 9, 2006, 15:25:12 ; Search time 25.423 Seconds  
(without alignments)  
614.628 Million cell updates/sec

Title: US-09-811-367b-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLLEPTATQAQN.....GLQSSCEVPLHGCKKRL 189

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/PCrus\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	525.5	51.4	188 2 US-08-722-126A-5	Sequence 5, Appli
2	525.5	51.4	188 4 PCT-US95-04258-5	Sequence 5, Appli
3	55	5.4	188 1 US-08-486-715-5	Sequence 5, Appli
4	55	5.4	188 1 US-08-486-719-5	Sequence 5, Appli
5	55	5.4	188 1 US-08-476-100-5	Sequence 5, Appli
6	55	5.4	188 1 US-08-286-767-3	Sequence 3, Appli
7	55	5.4	188 2 US-08-475-749-5	Sequence 5, Appli
8	54.5	5.3	188 2 US-10-104-047-2380	Sequence 2380, Ap
9	53.5	5.2	188 2 US-09-328-352-7291	Sequence 7291, Ap
10	52	5.1	188 2 US-09-122-443-14	Sequence 14, Appli
11	52	5.1	188 2 US-09-558-089-14	Sequence 14, Appli
12	52	5.1	188 2 US-09-558-087-14	Sequence 14, Appli
13	52	5.1	188 2 US-09-558-474-14	Sequence 14, Appli
14	52	5.1	188 2 US-09-123-482A-1	Sequence 1, Appli
15	50.5	4.9	188 2 US-09-543-681A-7232	Sequence 7232, Ap
16	50	4.9	188 2 US-09-489-039A-9728	Sequence 9728, Ap
17	48.5	4.7	188 2 US-07-757-022B-32	Sequence 32, Appli
18	48	4.7	188 2 US-09-270-767-36523	Sequence 36523, A
19	48	4.7	188 2 US-09-270-767-51740	Sequence 51740, A
20	47	4.6	188 2 US-09-206-935-19	Sequence 19, Appli
21	47	4.6	188 2 US-09-206-936-19	Sequence 19, Appli
22	47	4.6	188 2 US-07-145-002B-12	Sequence 12, Appli
23	47	4.6	188 2 US-07-145-002B-22	Sequence 22, Appli
24	47	4.6	188 2 US-06-256-204C-12	Sequence 12, Appli
25	47	4.6	188 2 US-06-256-204C-22	Sequence 22, Appli
26	47	4.6	188 2 US-09-919-497-73	Sequence 73, Appli
27	46	4.5	188 2 US-09-248-796A-23410	Sequence 23410, A

28	46	4.5	189 2 US-09-487-792-8	Sequence 8, Appli
29	46	4.5	189 2 US-09-322-409-111	Sequence 111, App
30	46	4.5	189 2 US-09-908-594-8	Sequence 8, Appli
31	46	4.5	189 2 US-09-451-527-111	Sequence 111, App
32	46	4.5	189 2 US-09-198-452A-1169	Sequence 1169, Ap
33	45.5	4.4	189 2 US-09-303-518D-232	Sequence 232, App
34	44.5	4.3	189 1 US-08-026-758-16	Sequence 16, Appli
35	44	4.3	188 2 US-09-252-991A-20399	Sequence 20399, A
36	44	4.3	188 2 US-09-270-767-37708	Sequence 37708, A
37	44	4.3	188 2 US-09-451-527-168	Sequence 168, App
38	44	4.3	189 2 US-08-026-758-17	Sequence 17, Appli
39	43.5	4.3	189 1 US-08-487-792-7	Sequence 7, Appli
40	43.5	4.3	189 2 US-09-908-594-7	Sequence 7, Appli
41	43.5	4.3	189 2 US-09-902-540-14285	Sequence 14285, A
42	43.5	4.3	188 2 US-09-252-991A-29853	Sequence 29853, A
43	43	4.2	188 2 US-09-252-991A-31741	Sequence 31741, A
44	43	4.2	188 2 US-09-527-376-2	Sequence 2, Appli
45	43	4.2		

ALIGNMENTS

RESULT 1  
US-08-722-126A-5  
Sequence 5, Application US/08722126A  
Patent No. 6034227  
GENERAL INFORMATION:  
APPLICANT: PECHT, Israel  
APPLICANT: GUTHMANN, Marcelo D.  
APPLICANT: TAL, Michael  
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,126A  
FILING DATE: 08-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04258  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 109257  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: PECHT=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-722-126A-5  
Query Match 51.4%; Score 525.5; DB 2; Length 188;  
Best Local Similarity 53.5%; Pred. No. 1.7e-48;







COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/122,443  
FILING DATE: 24-JUL-1998  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/053,765  
FILING DATE: 25-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0758K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-122-443-14

Query Match 5.1%; Score 52; DB 2; Length 188;  
Best Local Similarity 20.5%; Pred. No. 1.4e+03;  
Matches 27; Conservative 17; Mismatches 54; Indels 34; Gaps 3;

QY 44 GLTAVLTLVLYQWILCOGSN-----YSTCASCPSG--- 75  
DB 30 GLTILVLEIVEKELCNQNSDCMNNDDALAENNLKLPETIQNDGCTGYNOETCLLK 89  
QY 76 -PDRMKYGNHCYFVSVEKDNSSLEFCLARDSHLVTIDNOEMS-----LIQVFLSEA 129  
DB 90 ISSGLLEHYSHYLEYMKNNLDKNDKARVLRDTETLIHFNOEVKDLHKIVLPTPIISNA 149  
QY 130 FCWIGLRNNSGW 141  
DB 150 LITDKLESQKEW 161

RESULT 11  
US-09-558-089-14  
Sequence 14, Application US/09558089  
Patent No. 6479634  
GENERAL INFORMATION:  
APPLICANT: Bazan, J. Fernando  
TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/558,089  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/122,443

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0758K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-558-089-14

Query Match 5.1%; Score 52; DB 2; Length 188;  
Best Local Similarity 20.5%; Pred. No. 1.4e+03;  
Matches 27; Conservative 17; Mismatches 54; Indels 34; Gaps 3;

QY 44 GLTAVLTLVLYQWILCOGSN-----YSTCASCPSG--- 75  
DB 30 GLTILVLEIVEKELCNQNSDCMNNDDALAENNLKLPETIQNDGCTGYNOETCLLK 89  
QY 76 -PDRMKYGNHCYFVSVEKDNSSLEFCLARDSHLVTIDNOEMS-----LIQVFLSEA 129  
DB 90 ISSGLLEHYSHYLEYMKNNLDKNDKARVLRDTETLIHFNOEVKDLHKIVLPTPIISNA 149  
QY 130 FCWIGLRNNSGW 141  
DB 150 LITDKLESQKEW 161

RESULT 12  
US-09-558-087-14  
Sequence 14, Application US/09558087  
Patent No. 6495667  
GENERAL INFORMATION:  
APPLICANT: Bazan, J. Fernando  
TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/558,087  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/053,765  
FILING DATE: 25-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0758K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid

```

; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-558-087-14

```

Query Match	5.1%	Score 52	DB 2	Length 188
Best Local Similarity	20.5%	Pred. No. 1.4e+03		
Matches 27	Conservative 17	Mismatches 54	Indels 34	Gaps 3

QY 44 GLTTAVLLSLVLTQWILLCOGSN-----YSTASCPSC--- 75  
 Db 30 GLITHTVLMEIVEMRKELCNGNSDCMNDALANNILKLPEIGRNDGCVGTGNGEITCLK 89  
 QY 76 -PBRMKNYGHGCHYFVEEEMKDNMSLSEFCIARDSHLYITNDQEMS-----LQVFLSEA 125  
 Db 90 ISSGLLEHYSLIYEMKNNLKDKKKARVLDQRTETLIHFQGVKDKIKVLEPPIISNA 149  
 QY 130 FCWIGLRNNSGW 141  
 Db 150 LLTDTKLESQKEW 161

RESULT 13  
US-09-558-474-14  
; Sequence 14, Application US/09558474  
; Patent No. 6835825

1 GENERAL INFORMATION:  
2 APPLICANT: Bazan, J. Fernando  
3 TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
4  
5 NUMBER OF SEQUENCES: 16  
6  
7 CORRESPONDENCE ADDRESS:

ADDRESS: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

44 GLLTAVLSEVLLQYMIICQGSN-----YSTACAPSC--- 75

```

Db      30 GLITHTVLMIEVREKRLCSGNSDCNNNDALAEENLKP:EIQRDGCXYGTGYNDEICLLK  89
QY      76 -PRRMKKNHCHCYFSEVEEKKMNSLSEPCLRDSHLVTITGNQMS-----ILQVFLSEA  129
           :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      90 ISSGGLFHSYLEYEMKNNIKDKKKRKAVALQRDTETLIHINQGVKDLHKI VLPETPSNA  149
           :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      130 FCMIGIRANSGW  141
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      150 LITDKLKLSQKEW  161
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 14  
US-09-123-492A-1  
; Sequence 1, Application US/09123492A  
Date: 09/09/2009

```

: GENERAL INFORMATION:
: APPLICANT: KLINEFELTER, GARY
: TITLE OR INVENTION: METHOD FOR EVALUATING AND AFFECTING MALE FERTILITY
: FILE REFERENCE: KLINEFELTER=1B
: CURRENT APPLICATION NUMBER: US/09/123,492A
: CURRENT FILING DATE: 1998-07-28
: PRIOR APPLICATION NUMBER: 08/593,677
: PRIOR FILING DATE: 1997-01-29
: PRIOR APPLICATION NUMBER: PCT/US97/01725
: PRIOR FILING DATE: 1997-01-29
: PRIOR APPLICATION NUMBER: 60/082,753
: PRIOR FILING DATE: 1998-04-23
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 169
: TYPE: PRT
: ORGANISM: Human DJ-1
: US-09-123-492A-1

```

Query Match	5.1%;	Score 52;	DB 2;	Length 189;
Best Local Similarity	31.9%;	Pred. No. 1.4e+03;		
Matches	23;	Conservative	9;	Mismatches 26;
			Indels	14;
			Gaps	4

```

Oy      4 GLLTAIVL--SVLYQWILCGSSNYSSTASCSPSCDPRMKYGNHCYFYSVEKQM----- 96
Db      100 GLIAALCAGFTALIAIEICG-SKVTY---HPLADKRMNGNGHTYSNRERKGLILTS 156
Oy      97 ---NSLSIEGLA 105
Db      156 RRGPTSFEEFALA 167

```

RESULT 15  
US-09-543-681A-7232  
; Sequence 7232, Application US/09543681A

```

: GENERAL INFORMATION:
: APPLICANT: GARY BRETON
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
: TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTICS
: FILE REFERENCE: 2709.1002-001
: CURRENT APPLICATION NUMBER: US/09/543,681A
: CURRENT FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: US 60/128,706
: PRIOR FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 8344
: SEQ ID NO 7232
: LENGTH: 188
: TYPE: PRT
: ORGANISM: Proteus mirabilis
: US-09-543-681A-7232

```

Query Match	4.9%;	Score 50.5;	DB 2;	Length 188;
Best Local Similarity	21.0%;	Pred. No. 2e+03;		
Matches 30;	Conservative 16;	Mismatches 56;	Indels 41;	Gaps 8
15 ATGAGDYGQQKSSSSKPCSCVAITLGLTAVLZSVLXQWILCGSNYSTC-----	69			

15 ATQAQNDYGHQKSSSKPSCSLVAITLGLTAVLLSVLLYQWILCOGSNSTC----- 69

```
Db      50 ALKSQGD-GQVIVYLEBQP-CQCCGA-----DLVLRQKFGMFIGC--SNYPACEHIEQ 99
QY      70 -----ASCSPCP-----DRMMKYGNHCY-----YFSVEEKDWNSSLEFCLARDS 108
Db      100 IDKPDETVHCHPQCEKSKLIQKSRFGKIFACNOYBECQFVUNNKFINGECEYC----- 154
QY      109 HLLVITDNOEMSLLOVFLSEAPC 131
Db      155 HYPLEMEKRSSQGVRLVCASKLC 177
```

Search completed: January 9, 2006, 15:37:59  
Job time : 26.423 sec8

**This Page Blank**

**Page 10**





PS Disclosure; Fig 1; 44pp; English.

CC This is the amino acid sequence of human mast cell function- associated  
CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAW84198)  
CC encoding human MAFA can be obtained from myelogenous leukaemic cell line  
CC KU812 or cDNA derived from human lung tissue. The encoded protein is  
CC similar to the rat form (see AAW88277) having an intracellular domain  
CC containing a putative immunoreceptor tyrosine activation motif (ITAM) and  
CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see  
CC AAW8266-67) of human MAFA have been identified. Polypeptides and  
CC synthetic peptides (see AAW8258-64) based on these truncated MAFA  
CC proteins can be used in methods for the treatment of inflammatory and  
CC allergic diseases, and tumour growth

CC Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVITYSMLELPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60  
DB 1 MTDVITYSMLELPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60  
QY 61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSEBKDNSSLFECCLARDSHLLVITDNOEMS 120  
DB 61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSEBKDNSSLFECCLARDSHLLVITDNOEMS 120  
QY 121 LLOVFLSEAFQWIGLRNNGRWEDGSPINFSRISNSFVOTCGAINNKGLOASSCEVPL 180  
DB 121 LLOVFLSEAFQWIGLRNNGRWEDGSPINFSRISNSFVOTCGAINNKGLOASSCEVPL 180  
QY 181 HGVCCKVRL 189  
DB 181 HGVCCKVRL 189

RESULT 2

ID AAE11759 standard; protein; 189 AA.

XX AAE11759;

DT 18-DEC-2001 (first entry)

DE Human mast cell function associated antigen (MAFA) protein.

XX Human; pharmaceutical composition; mast cell function associated antigen;  
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
KW immunosuppressive; cytostatic.

XX Homo sapiens.

FN WO200170805-A2.

XX 27-SEP-2001.

PF 16-MAR-2001; 2001WO-US008596.

FR 17-MAR-2000; 2000US-0190716F.

PA (GEMI-) GEMINI SCI INC.

PI Takahashi N, Mikayama T;

DR WPI; 2001-611482/70.

DR N-PSDB; AAD18734.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic  
PT activity of natural killer cell or T-cell, comprises an agent that binds  
PT to mast cell function-associated antigen ligand on target cell.

PS Claim 10; Page 18; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising  
CC an agent which specifically binds to a mast cell function associated  
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA  
CC ligand and a pharmaceutically acceptable excipient. The invention is  
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA  
CC binding to a ligand on a target cell, by contacting the pharmaceutical  
CC composition in vitro, ex vivo or in vivo by administering the composition  
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
CC on the target cell. The agent or the composition is useful for treating a  
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
CC tumour cell. The invention is also useful for inhibiting an activity of  
CC NK cell or a T-cell. The present sequence is human MAFA protein

XX Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 4; Length 189;  
Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVITYSMLELPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60  
DB 1 MTDVITYSMLELPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60  
QY 61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSEBKDNSSLFECCLARDSHLLVITDNOEMS 120  
DB 61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSEBKDNSSLFECCLARDSHLLVITDNOEMS 120  
QY 121 LLOVFLSEAFQWIGLRNNGRWEDGSPINFSRISNSFVOTCGAINNKGLOASSCEVPL 180  
DB 121 LLOVFLSEAFQWIGLRNNGRWEDGSPINFSRISNSFVOTCGAINNKGLOASSCEVPL 180  
QY 181 HGVCCKVRL 189  
DB 181 HGVCCKVRL 189

RESULT 3

ID ADD25635 standard; protein; 189 AA.

AC ADD25635;

DT 15-JAN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated protein #95.

XX Binding domain; immunoglobulin; fusion protein; cytostratic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neutroprotective; hinge region; immunoglobulin heavy chain.

KW CH2 constant region; CH3 constant region; 19G1.

KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;

KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

OS US2003118592-A1.

PN 26-JUN-2003.

XX 25-JUN-2002; 2002US-00207655.

PF 17-JAN-2001; 2001US-0367358P.

PR 17-JAN-2002; 2002US-00053530.

PR 03-JUN-2002; 2002US-0385691P.

PA (GENE-) GENE-CRAFT INC.

PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 XX WPI, 2003-801317/75.  
 DR  
 XX  
 PT New binding domain-immunoglobulin fusion protein, useful for treating a  
 PT subject having or suspected of having a malignant condition or a B-cell  
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
 PS  
 XX  
 PS Disclosure; SEQ ID NO 196; 157bp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein  
 CC comprising a binding domain polypeptide that is fused to an  
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
 CC CH2 constant region polypeptide that is fused to the hinge region  
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
 CC polypeptide that is fused to the CH2 constant region polypeptide. The  
 CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin  
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
 CC region polypeptide; derived from (a) having 3 or more cysteine residues;  
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
 CC immunoglobulin hinge region polypeptide contains no more than one  
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
 CC capable of at least one immunological activity comprising antibody  
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
 CC binding domain polypeptide is capable of specifically binding to an  
 CC antigen. Also included are an isolated polynucleotide encoding the  
 CC binding domain-immunoglobulin fusion protein, a recombinant expression  
 CC construct comprising the polynucleotide (operably linked to a promoter),  
 CC a host cell transformed or transfected with a recombinant expression  
 CC construct, producing the binding domain-immunoglobulin fusion protein, a  
 CC pharmaceutical composition comprising the binding domain-immunoglobulin  
 CC fusion protein or polynucleotide and a carrier, and treating a subject  
 CC having or suspected of having a malignant condition or a B-cell disorder.  
 CC The binding domain-immunoglobulin fusion protein is useful for treating a  
 CC subject having or suspected of having a malignant condition or a B-cell  
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
 CC myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple  
 CC sclerosis or autoimmune disease. The present sequence is a binding domain  
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
 CC sequence data for this patent formed part of the printed specification  
 CC and is also available in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not  
 CC identified the sequences in the printed specification by their SEQ ID  
 CC number therefore none of the sequences can be explicitly identified.

XX Sequence 189 AA:

Query Match 98.4%; Score 1007; DB 7; Length 189;

Best Local Similarity 98.4%; Pred. No. 1.3e-96;  
 Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVSIYSMLPTATQANDYGPQKSSSKPSCGLVAITLGLTAVALLSVLYQWIL 60  
 DB 1 MTDVSIYSMLPTATQANDYGPQKSSSKPSCGLVAITLGLTAVALLSVLYQWIL 60  
 QY 61 CQGSNSTSTCASCPSPRMWKYGNHCYFVSVEKDMNSLFFCLARDSHLLVITDNOEMS 120  
 DB 61 CQGSNSTSTCASCPSPRMWKYGNHCYFVSVEKDMNSLFFCLARDSHLLVITDNOEMS 120  
 QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLOASSCEVPL 180  
 DB 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLOASSCEVPL 180  
 QY 181 HGVCCKVRL 189  
 DB 181 HGVCCKVRL 189

RESULT 4  
 ADY19892  
 ID ADY19892 standard; protein; 189 AA.  
 XX  
 AC ADY19892;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE PRO polypeptide SEQ ID NO 5698.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
 KW Antithyroid; Antidiabetic; Nephrotoxic; CNS-Gen.; Hepatocrotropic;  
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiaesthetic;  
 KW Antiallergic; diagnosis.

XX Homo sapiens.  
 XX  
 PN MO2005016962-A2.  
 XX  
 PD 24-FEB-2005.

XX 11-AUG-2004; 2004MO-US026249.  
 XX  
 PF 11-AUG-2003; 2003US-0493546P.

XX 11-AUG-2003; 2003US-0493546P.  
 XX  
 PA (GENTH ) GENENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
 XX WPI, 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 5698; 158bp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO  
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
 CC composition, and method are useful for diagnosing and treating an immune  
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 189 AA:

Query Match 98.4%; Score 1007; DB 9; Length 189;

Best Local Similarity 98.4%; Pred. No. 1.3e-96;  
 Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVSIYSMLPTATQANDYGPQKSSSKPSCGLVAITLGLTAVALLSVLYQWIL 60  
 DB 1 MTDVSIYSMLPTATQANDYGPQKSSSKPSCGLVAITLGLTAVALLSVLYQWIL 60  
 QY 61 CQGSNSTSTCASCPSPRMWKYGNHCYFVSVEKDMNSLFFCLARDSHLLVITDNOEMS 120  
 DB 61 CQGSNSTSTCASCPSPRMWKYGNHCYFVSVEKDMNSLFFCLARDSHLLVITDNOEMS 120  
 QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLOASSCEVPL 180  
 DB 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLOASSCEVPL 180  
 QY 181 HGVCCKVRL 189  
 DB 181 HGVCCKVRL 189  
 RESULT 5  
 AAE11760  
 ID AAE11760 standard; protein; 188 AA.  
 XX  
 AC AAE11760;

```
XX 18-DEC-2001 (first entry)
XX
XX Mouse mast cell function associated antigen (MAFA) protein.
DE
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 64..188
XX FT Domain /note="Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCT INC.
XX
XX Takehashi N, Miyayama T;
XX PI
XX MPI: 2001-611482/70.
XX DR N-PSDB; MAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX PT activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX CC ligand and a pharmaceutically acceptable excipient. The invention is
XX CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX CC binding to a ligand on a target cell, by contacting the pharmaceutical
XX CC composition in vitro, ex vivo or in vivo by administering the composition
XX CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX CC on the target cell. The agent or the composition is useful for treating a
XX CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX CC tumour cell. The invention is also useful for inhibiting an activity of
XX CC NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
XX Sequence 188 AA:
SQ
Query Match 53.6%; Score 548.5; DB 4; Length 188;
Best Local Similarity 55.6%; Pred. No. 16-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
QY 1 MTDSTIYMLPTPTAQNNDYGPQOKSSSKPSCGLVATLGLTAVLSVLLYQWL 60
DB 1 MADSIYSTLELPEAPPOVODESRWKLKAVLRPHLSRFAMVALGLTIVILMSLTYQRTL 60
QY 61 CGGSNYSTCASCPCSPDRMKYGNHCYFYSVEKDMNSLBEFLARDSHLVTITNOEMS 120
DB 61 CGGSNDSTCSHCPSCPILMTNRNGSHCYFSMEKDMNSLKFCAKGSHTLTFPNDQGVK 120
QY 121 LLOVFLSEAFQWIGLRNNSGWRMEDGSPUNFSRISNSFVQTGAINKXGLQASSCEVPL 180
DB 121 LFGELYGDFWYIGLRNIDGWRMEGSPALSL-RILTNLSIQCGAIIHRGQLQASSCEVAL 179
QY 181 HGVCKKV 187
DB 180 QWICKKV 186
```

```
RESULT 6
AAR77033
ID AAR77033 standard; protein, 188 AA.
XX
XX AAR77033;
XX
XX 01-FEB-1996 (first entry)
XX
XX Mammalian mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
XX identification; screening; inflammation; inflammatory; allergy; allergic;
XX prevention.
XX
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX (RYCU/) RYCUS A.
XX
XX Pecht I, Gutmann MD, Tal M;
XX
XX MPI: 1995-366356/47.
XX DR N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX PT useful for screening for ligands of MAFA which are useful for prevention
XX of inflammatory and allergic reactions.
XX
XX Claim 12; Page 37; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX CC produced by recombinant techniques for use in the ligand- screening
XX CC assay. The ligands that are identified may be used alone or in
XX CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
XX Sequence 188 AA:
SQ
Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 2.5e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSTIYMLPTPTAQNNDYGPQOKSSSKPSCGLVATLGLTAVLSVLLYQWL 60
DB 1 MADSIYSTLELPEAPPOVODESRWKLKAVLRPHLSRFAMVALGLTIVILMSLTYQRTL 60
QY 61 CGGSNYSTCASCPCSPDRMKYGNHCYFYSVEKDMNSLBEFLARDSHLVTITNOEMS 120
DB 61 CGSGKGFMCQCSRCRPNIMMNGSHCYFSMEKDMNSLKFCAKGSHTLTFPNDQGVN 120
QY 121 LLOVFLSEAFQWIGLRNNSGWRMEDGSPUNFSRISNSFVQTGAINKXGLQASSCEVPL 180
DB 121 LFOEYVGBDFWYIGLRNIDGWRMEDGSPALSLS-IISNSVVOKCGTIIHRGQLQASSCEVAL 179
QY 181 HGVCKKV 187
DB 180 QWICKKV 186
RESULT 7
AAM8277
ID AAM8277 standard; protein, 188 AA.
XX
XX AAM8277;
AC AAM8277;
```

XX	29-MAR-1999	(first entry)
DT		
XX		
DE		Rat mast cell function-associated antigen (MAFA).
XX		
KW		Mast cell function-associated antigen; MAFA; splice variant; rat;
XX		
KX		Inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX		
OS		Rattus sp.
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	82..84
FT		/note="Asn is N-glycosylated"
FT	Modified-site	97..99
FT		/note="Asn is N-glycosylated"
XX		
PN	W09854209-A2.	
XX		
PD	03-DEC-1998.	
XX		
PF	29-MAY-1998;	98WO-GB001572.
XX		
PR	31-MAY-1997;	97GB-00011148.
XX		
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX		
PI	Hewlett EL, Lamere MBAC, Lamont A, Williams DH;	
XX		
DR	WPI: 1999-059806/05.	
XX		
DR	N-PSDB; AAV84222.	
XX		
PT		New polypeptide having a sequence corresponding to human mast cell
XX		
PT		function-associated antigen - useful in forming and manufacturing
XX		
PT		pharmaceutical compositions in the treatment of inflammatory and allergic
XX		
XX		diseases, and tumour growth.
PS		
PS	Disclosure; Fig 4; 44pp; English.	
XX		
CC		This is the amino acid sequence of rat mast cell function-associated
XX		
CC		antigen (MAFA), a type II membrane glycoprotein found on mast cells and
XX		
CC		basophils. The invention relates to cloning of the human MAFA molecule
XX		
CC		(see AAV88265) and to the discovery of splice variants (see AAV88266-67)
XX		
CC		of human MAFA that are not found in rat. Polypeptides and synthetic
XX		
CC		peptides (see AAV88258-64) based on human MAFA and human truncated MAFA,
XX		
CC		and polynucleotides encoding them, can be used in methods for the
XX		
CC		treatment of inflammatory and allergic diseases (e.g. rheumatoid
XX		
CC		arthritis and asthma), and tumour growth
XX		
SQ	Sequence 188 AA;	

Query Match	51.4%;	Score 525.5;	DB 2;	Length 188;
Best Local Similarity	53.5%;	Pred. No. 2.5e-45;		
Matches	100;	Conservative	29;	Mismatches 57;
				Indels 1;
				Gaps 1;
Qy	1	MTDSVIYSMLDELPTAQAGNDYGPQOKSSSSKPSCSCLVAITLGLTAVLLSVLLYQWIL	60	
Db	1	MADNSIYSITLIELPAPRIVQDDSRMKVKAVLHPRCVSYLVWVVLGLITVILMSILLYQRTL	60	
Qy	61	CCGSNYSITASPCSPCDPMKKYKGNHCYPSVEKXQMNSSLERCLARDSHLIVITNOMS	120	
Db	61	CCGSYKGFMCSSQCSRCPNLMWRNGSHCYTYSMEKRDWNSLKFCAKDGSHLTFPPNQGVN	120	
Qy	121	LLOVFLSEAFPCWIGLRNNSGMRWEDGSPUNFGRISNSFPVOTCGAINKNGLOASSCEVPL	180	
Db	121	LPOEYVGEDFPYVIGLRDIDGMRWEDGPALSTLSILSNSVYKCGTITHRGILHAASSCEVAL	179	
Qy	181	HGVCKKV	187	
Db	180	QWICEKV	186	
RESULT 8				
AAE11761				

ID AAE11761 standard; protein; 188 AA.  
 AC AAE11761;  
 XX  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Rat mast cell function associated antigen (MAFA) protein.  
 XX  
 XX Rat; pharmaceutical composition; mast cell function associated antigen;  
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
 XX immunosuppressive; cytostatic.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN WO200170805-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 16-MAR-2001; 2001WO-US008596.  
 PF  
 PR 17-MAR-2000; 2000US-0190716P.  
 XX  
 XX  
 PA (GEMI-) GEMINI SCI INC.  
 XX  
 XX  
 PI Takahashi N, Mikayama T;  
 XX  
 DR WPI: 2001-611482/70.  
 DR N-PSDB; AADI8736.  
 XX  
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic  
 PT activity of natural killer cell or T-cell, comprises an agent that binds  
 PT to mast cell function-associated antigen ligand on target cell.  
 XX  
 XX  
 PS Example 1; Page 19; 49pp; English.  
 XX  
 XX  
 CC The present invention relates to a pharmaceutical composition comprising  
 CC an agent which specifically binds to a mast cell function associated  
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA  
 CC ligand and a pharmaceutically acceptable excipient. The invention is  
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA  
 CC binding to a ligand on a target cell, by contacting the pharmaceutical  
 CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is rat MAFA protein

Query Match	51.4%	Score 525.5	DB 4	Length 188
Best Local Similarity	53.5%	Pred. No. 2.5e-46		
Matches 100	Conservative	29	Mismatches 57	Indels 1
Qy	1	MTDSVIYKMLEPTITQANDYGPQOKSSSKPSCSCVAILTGITLAVLSVLYQWIL	60	
Db	1	MADNSIYSTLEIPALPRVODDSRMVKVLAHRPCVSYVMALGLTITVMSLLYQRTL	60	
Qy	61	CGSGSYSTCASCPGCPDRMKYKGNHCYFSEYSEKDMNSLSEFCLARDSHLAVITDNOEMS	120	
Db	61	CGSGSGFMCSQSCRCPNLMMRWGSCYIFSMERKMNSLKEFCDKSGHLLTFPNQGVN	120	
Qy	121	LLQVFLSEAFWIGLRNNSGWRMEDGSPINFGRISSNSFVQTGAINKGLQASSCEVPL	180	
Db	121	LFQEVYEGDFYVITGLRIDIGWRMEDGPAISLS-ILSNSVVGCGTIIHRCGLHAASCEVAL	179	
Qy	181	HGVCKKV	187	
Db	180	QWICEKV	186	

```
RESULT 9
AEA89021
ID AEA89021 standard; protein; 188 AA.
XX
AC AEA89021;
XX
DT 25-AUG-2005 (first entry)
XX
DE Chicken MHC C-type lectin receptor, B-1ec protein.
XX
KW Transgenic animal; disease-resistance; gene therapy; screening; B-1ec;
KW lectin; major histocompatibility complex; receptor.
XX
OS Gallus gallus.
XX
PN WO2005054280-A2.
XX
PD 16-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-GB005108.
XX
PR 05-DEC-2003; 2003GB-00028248.
XX
PA (OXFORD BIOMEDICA UK LTD.
PA (ANIM-) INST ANIMAL HEALTH.
XX
PI Carrol J M, Kaufman J, Mitrophanous K;
XX
DR WPI; 2005-425385/43.
XX
DR N-PSDB; AEA89020.
XX
PT Producing transgenic animal having modified resistance to disease, by
PT introducing retrovirus having polynucleotide sequence encoding protein
PT that modifies disease resistance of animal, into cell of animal.
XX
PS Disclosure; SEQ ID NO 8; 90pp; English.
XX
SS The present invention relates to a method of producing transgenic animal
SS having modified resistance to a disease. The method involves introducing
SS retrovirus having polynucleotide sequence encoding protein that modifies
SS disease resistance of animal, into cell of animal. The invention is
SS useful for screening proteins capable of modifying resistance of an
SS animal to a disease, for producing transgenic bird and fish and also
SS useful in gene therapy. The present sequence is the chicken major
SS histocompatibility complex (MHC) C-type lectin receptor, B-1ec protein.
SS This sequence is used to produce a transgenic animal having modified
SS resistance to a disease.
XX
SQ Sequence 188 AA;
XX
Query Match 16.5%; Score 168.5; DB 9; Length 188;
Beet Local Similarity 27.3%; Pred. No. 5e-09; 77; Indels 27; Gaps 6;
Matches 48; Conservative 24; Mismatches 77; Indels 27; Gaps 6;
QY 26 QKSSSSKPSKSC-----SCLVAITLGLTAVLTLVLYQWILCOGSNYSTCASCSPCPDRWM 80
DB 17 RRGSGSRGCTVTFQULMAVFTVLITANAFVQAFQ-----PHQPCAQCPFWMI 67
QY 81 KYGNHCYFVSVEKCMNSLLEFCCLARDSHLVTYTNQENSLQVPLSEAFCTIGLRNNS- 139
DB 68 GFRGCKYFSEBDESSQNNCSALGASLAVFDSAEDLSFTMRKXGSSPHWVGLSRGK 127
QY 140 ---GWMWEDGSLNFRISNSF-VQ---TCGAINKNGCLQASCEVPLNHCVCCKVTL 189
DB 128 EHPWEMVNRSP-----SHLPVOGQDGLCAVLGADGLSSSHCSARRNWCYKPAL 177
RESULT 10
AAU19837
ID AAU19837 standard; protein; 189 AA.
XX
AC AAU19837;
XX
```

```
XX
DT 04-DEC-2001 (first entry)
XX
DE Human novel extracellular matrix protein, Seg ID No 487.
XX
KW Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
KW antianemic; antineumatic; antisclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antifalmeira; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancer; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.
XX
OS Homo sapiens.
XX
PN WO20015368-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001348.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0188874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229519P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0231414P.
```

```

PR 01-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251031P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-465572/50.
XX
DR N-PSTB: AAS31408.
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
XX proteins, used in preventing, treating or ameliorating a disorder, e.g.
XX Alzheimer's and Parkinson's diseases and cancers.
XX
PS Claim 11, SEQ ID NO 487; 577pp; English.
XX
CC The invention relates to isolated nucleic acid molecules encoding novel
XX human secreted extracellular matrix proteins (SPs). The polynucleotides
XX and proteins are used to prevent, treat a medical condition in e.g.
XX humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For
XX example, disorders associated with decreased expression of SPs. The SP
XX polynucleotide or a vector expressing them may be administered to treat
XX diseases by gene therapy. Antisense molecules may be administered to down
XX regulate expression of SPs by binding with the cells own genes and
XX preventing their expression. The polynucleotides may also be used as DNA
XX probes in diagnostic assays. The SPs may also be used as antigens to
XX produce antibodies and to identify modulators (agonists and antagonists)
XX of the SPs. The anti-(SP) antibodies and antagonists may also be used to
XX down regulate expression and activity of SP and as diagnostic agents for
XX detecting the presence of SPs in samples. The disorders include for
XX example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency
XX virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis),
XX cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of
XX the breast or liver, Sezary syndrome and Gaucher's disease), neurological
XX diseases (e.g. Alzheimer's disease, Parkinson's disease) Cardio-
XX /cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina),
XX infections caused by bacteria, viruses and fungi and ocular disorders
XX (e.g. corneal infections). Other uses include wound healing, maintenance
XX of organs before transplantation, support of cell culture of primary
XX
Query Match      16.1%; Score 165; DB 4; Length 189;
Best Local Similarity 28.8%; Pred. No. 1.2e-08;
Matches 36; Conservative 24; Mismatches 53; Indels 12; Gaps 5
QY 69 CASCPSS-CPDRMKXGNHCYYFVSVEKDWNSLFECLARDSHLVITTONQMSLLQVPIS 127
DB 68 CIKCBAPEPDMLLYGRCKCYFSEBPDMNTGROYCHTHEAVLAIVIOSKELEFFPKF-T 126
QY 128 EAFCHTIGLRN-NSGMRWEDGSPLNRSRISNSFV---QTGAINKNGIQASSCEVPLHG 182
DB 127 RREPPIGIRRVGDDEPHWNGBPFD-----PDTFTTAGGEVCVFEPTRLVSYTECIATRP 181
QY 183 VCKKV 187
DB 182 VCSKM 186
XX
RESULT 11
ID ABBI17910 standard; protein; 189 AA.
XX
```

AC ABB17910;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Human nervous system related polypeptide SEQ ID NO 6567.  
XX  
KW Human; nootropic; neuroprotective; cyostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antischizoid; antianaemic; antidiabetic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antifungal;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
PN WO200159063-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001334.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-022679P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-022668P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0228287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229309P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0232402P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-023497P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235835P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241825P.  
PR 20-OCT-2000; 2000US-0242221P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250391P.



PR 01-DEC-2000; 2000US-0251160P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI, 2001-541565/60.  
DR N-PSDB; ABA14236.  
XX  
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating nervous system cancers  
PT and metastases.  
XX  
XX Claim 11; SEQ ID NO 6567; 1701pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins  
CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from Wipo at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
XX  
XX Sequence 189 AA;  
SQ  
Query Match 16.1%; Score 165; DB 4; Length 189;  
Best Local Similarity 28.8%; Pred. No. 1.2e-08;  
Matches 36; Conservative 24; Mismatches 53; Indels 12; Gaps 5;  
QY 69 CASCPS-CPDRMKYGNHCYFVSVEKDNNSLEFCLARDSHLVTIDNQMSLQVFLS 127  
DB 68 CIRCEACCPEDWILYGRKCYFFSEPPDWTGRCYCHTHAVLAVIOSQLELMFKF-T 126  
QY 128 EARCWIGLRN-NSGWRWEDSPINFRISSNFV---QTCGAINKNGLOASSCEVPLHG 182  
DB 127 RREPWIGLRVGRGDFHVMVNGSPFD-----PDTFIAGPGEVFEPTRLVSTECIMTRPW 181  
QY 183 VCKKV 187  
DB 182 VCSKM 186  
RESULT 12  
ABP48057  
ID ABP48057 standard; protein; 189 AA.  
XX  
XX ABP48057;  
AC  
XX  
DT 23-AUG-2002 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 487.  
XX

KW Human; nocrotropic; neuroprotective; cytostatic; dermatological; virocidic;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatoprotective; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antilucifer; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
OS Homo sapiens.  
XX  
XX US2002042386-A1.  
XX  
XX 11-APR-2002.  
XX  
XX 17-JAN-2001; 2001US-00764870.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 07-JUL-2000; 2000US-0216647P.  
XX 07-JUL-2000; 2000US-0216880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225271P.  
XX 14-AUG-2000; 2000US-0225272P.  
XX 14-AUG-2000; 2000US-0225273P.  
XX 14-AUG-2000; 2000US-0225274P.  
XX 14-AUG-2000; 2000US-0225275P.  
XX 14-AUG-2000; 2000US-0225276P.  
XX 14-AUG-2000; 2000US-0225277P.  
XX 14-AUG-2000; 2000US-0225278P.  
XX 14-AUG-2000; 2000US-0225279P.  
XX 14-AUG-2000; 2000US-0225280P.  
XX 14-AUG-2000; 2000US-0225281P.  
XX 14-AUG-2000; 2000US-0225282P.  
XX 14-AUG-2000; 2000US-0225283P.  
XX 14-AUG-2000; 2000US-0225284P.  
XX 14-AUG-2000; 2000US-0225285P.  
XX 14-AUG-2000; 2000US-0225286P.  
XX 14-AUG-2000; 2000US-0225287P.  
XX 14-AUG-2000; 2000US-0225288P.  
XX 14-AUG-2000; 2000US-0225289P.  
XX 14-AUG-2000; 2000US-0225290P.  
XX 14-AUG-2000; 2000US-0225291P.  
XX 14-AUG-2000; 2000US-0225292P.  
XX 14-AUG-2000; 2000US-0225293P.  
XX 14-AUG-2000; 2000US-0225294P.  
XX 14-AUG-2000; 2000US-0225295P.  
XX 14-AUG-2000; 2000US-0225296P.  
XX 14-AUG-2000; 2000US-0225297P.  
XX 14-AUG-2000; 2000US-0225298P.  
XX 14-AUG-2000; 2000US-0225299P.  
XX 14-AUG-2000; 2000US-0225300P.  
XX 14-AUG-2000; 2000US-0225301P.  
XX 14-AUG-2000; 2000US-0225302P.  
XX 14-AUG-2000; 2000US-0225303P.  
XX 14-AUG-2000; 2000US-0225304P.  
XX 14-AUG-2000; 2000US-0225305P.  
XX 14-AUG-2000; 2000US-0225306P.  
XX 14-AUG-2000; 2000US-0225307P.  
XX 14-AUG-2000; 2000US-0225308P.  
XX 14-AUG-2000; 2000US-0225309P.  
XX 14-AUG-2000; 2000US-0225310P.  
XX 14-AUG-2000; 2000US-0225311P.  
XX 14-AUG-2000; 2000US-0225312P.  
XX 14-AUG-2000; 2000US-0225313P.  
XX 14-AUG-2000; 2000US-0225314P.  
XX 14-AUG-2000; 2000US-0225315P.  
XX 14-AUG-2000; 2000US-0225316P.  
XX 14-AUG-2000; 2000US-0225317P.  
XX 14-AUG-2000; 2000US-0225318P.  
XX 14-AUG-2000; 2000US-0225319P.  
XX 14-AUG-2000; 2000US-0225320P.  
XX 14-AUG-2000; 2000US-0225321P.  
XX 14-AUG-2000; 2000US-0225322P.  
XX 14-AUG-2000; 2000US-0225323P.  
XX 14-AUG-2000; 2000US-0225324P.  
XX 14-AUG-2000; 2000US-0225325P.  
XX 14-AUG-2000; 2000US-0225326P.  
XX 14-AUG-2000; 2000US-0225327P.  
XX 14-AUG-2000; 2000US-0225328P.  
XX 14-AUG-2000; 2000US-0225329P.  
XX 14-AUG-2000; 2000US-0225330P.  
XX 14-AUG-2000; 2000US-0225331P.  
XX 14-AUG-2000; 2000US-0225332P.  
XX 14-AUG-2000; 2000US-0225333P.  
XX 14-AUG-2000; 2000US-0225334P.  
XX 14-AUG-2000; 2000US-0225335P.  
XX 14-AUG-2000; 2000US-0225336P.  
XX 14-AUG-2000; 2000US-0225337P.  
XX 14-AUG-2000; 2000US-0225338P.  
XX 14-AUG-2000; 2000US-0225339P.  
XX 14-AUG-2000; 2000US-0225340P.  
XX 14-AUG-2000; 2000US-0225341P.  
XX 14-AUG-2000; 2000US-0225342P.  
XX 14-AUG-2000; 2000US-0225343P.  
XX 14-AUG-2000; 2000US-0225344P.  
XX 14-AUG-2000; 2000US-0225345P.  
XX 14-AUG-2000; 2000US-0225346P.  
XX 14-AUG-2000; 2000US-0225347P.  
XX 14-AUG-2000; 2000US-0225348P.  
XX 14-AUG-2000; 2000US-0225349P.  
XX 14-AUG-2000; 2000US-0225350P.  
XX 14-AUG-2000; 2000US-0225351P.  
XX 14-AUG-2000; 2000US-0225352P.  
XX 14-AUG-2000; 2000US-0225353P.  
XX 14-AUG-2000; 2000US-0225354P.  
XX 14-AUG-2000; 2000US-0225355P.  
XX 14-AUG-2000; 2000US-0225356P.  
XX 14-AUG-2000; 2000US-0225357P.  
XX 14-AUG-2000; 2000US-0225358P.  
XX 14-AUG-2000; 2000US-0225359P.  
XX 14-AUG-2000; 2000US-0225360P.  
XX 14-AUG-2000; 2000US-0225361P.  
XX 14-AUG-2000; 2000US-0225362P.  
XX 14-AUG-2000; 2000US-0225363P.  
XX 14-AUG-2000; 2000US-0225364P.  
XX 14-AUG-2000; 2000US-0225365P.  
XX 14-AUG-2000; 2000US-0225366P.  
XX 14-AUG-2000; 2000US-0225367P.  
XX 14-AUG-2000; 2000US-0225368P.  
XX 14-AUG-2000; 2000US-0225369P.  
XX 14-AUG-2000; 2000US-0225370P.  
XX 14-AUG-2000; 2000US-0225371P.  
XX 14-AUG-2000; 2000US-0225372P.  
XX 14-AUG-2000; 2000US-0225373P.  
XX 14-AUG-2000; 2000US-0225374P.  
XX 14-AUG-2000; 2000US-0225375P.  
XX 14-AUG-2000; 2000US-0225376P.  
XX 14-AUG-2000; 2000US-0225377P.  
XX 14-AUG-2000; 2000US-0225378P.  
XX 14-AUG-2000; 2000US-0225379P.  
XX 14-AUG-2000; 2000US-0225380P.  
XX 14-AUG-2000; 2000US-0225381P.  
XX 14-AUG-2000; 2000US-0225382P.  
XX 14-AUG-2000; 2000US-0225383P.  
XX 14-AUG-2000; 2000US-0225384P.  
XX 14-AUG-2000; 2000US-0225385P.  
XX 14-AUG-2000; 2000US-0225386P.  
XX 14-AUG-2000; 2000US-0225387P.  
XX 14-AUG-2000; 2000US-0225388P.  
XX 14-AUG-2000; 2000US-0225389P.  
XX 14-AUG-2000; 2000US-0225390P.  
XX 14-AUG-2000; 2000US-0225391P.  
XX 14-AUG-2000; 2000US-0225392P.  
XX 14-AUG-2000; 2000US-0225393P.  
XX 14-AUG-2000; 2000US-0225394P.  
XX 14-AUG-2000; 2000US-0225395P.  
XX 14-AUG-2000; 2000US-0225396P.  
XX 14-AUG-2000; 2000US-0225397P.  
XX 14-AUG-2000; 2000US-0225398P.  
XX 14-AUG-2000; 2000US-0225399P.  
XX 14-AUG-2000; 2000US-0225400P.  
XX 14-AUG-2000; 2000US-0225401P.  
XX 14-AUG-2000; 2000US-0225402P.  
XX 14-AUG-2000; 2000US-0225403P.  
XX 14-AUG-2000; 2000US-0225404P.  
XX 14-AUG-2000; 2000US-0225405P.  
XX 14-AUG-2000; 2000US-0225406P.  
XX 14-AUG-2000; 2000US-0225407P.  
XX 14-AUG-2000; 2000US-0225408P.  
XX 14-AUG-2000; 2000US-0225409P.  
XX 14-AUG-2000; 2000US-0225410P.  
XX 14-AUG-2000; 2000US-0225411P.  
XX 14-AUG-2000; 2000US-0225412P.  
XX 14-AUG-2000; 2000US-0225413P.  
XX 14-AUG-2000; 2000US-0225414P.  
XX 14-AUG-2000; 2000US-0225415P.  
XX 14-AUG-2000; 2000US-0225416P.  
XX 14-AUG-2000; 2000US-0225417P.  
XX 14-AUG-2000; 2000US-0225418P.  
XX 14-AUG-2000; 2000US-0225419P.  
XX 14-AUG-2000; 2000US-0225420P.  
XX 14-AUG-2000; 2000US-0225421P.  
XX 14-AUG-2000; 2000US-0225422P.  
XX 14-AUG-2000; 2000US-0225423P.  
XX 14-AUG-2000; 2000US-0225424P.  
XX 14-AUG-2000; 2000US-0225425P.  
XX 14-AUG-2000; 2000US-0225426P.  
XX 14-AUG-2000; 2000US-0225427P.  
XX 14-AUG-2000; 2000US-0225428P.  
XX 14-AUG-2000; 2000US-0225429P.  
XX 14-AUG-2000; 2000US-0225430P.  
XX 14-AUG-2000; 2000US-0225431P.  
XX 14-AUG-2000; 2000US-0225432P.  
XX 14-AUG-2000; 2000US-0225433P.  
XX 14-AUG-2000; 2000US-0225434P.  
XX 14-AUG-2000; 2000US-0225435P.  
XX 14-AUG-2000; 2000US-0225436P.  
XX 14-AUG-2000; 2000US-0225437P.  
XX 14-AUG-2000; 2000US-0225438P.  
XX 14-AUG-2000; 2000US-0225439P.  
XX 14-AUG-2000; 2000US-0225440P.  
XX 14-AUG-2000; 2000US-0225441P.  
XX 14-AUG-2000; 2000US-0225442P.  
XX 14-AUG-2000; 2000US-0225443P.  
XX 14-AUG-2000; 2000US-0225444P.  
XX 14-AUG-2000; 2000US-0225445P.  
XX 14-AUG-2000; 2000US-0225446P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225448P.  
XX 14-AUG-2000; 2000US-0225449P.  
XX 14-AUG-2000; 2000US-0225450P.  
XX 14-AUG-2000; 2000US-0225451P.  
XX 14-AUG-2000; 2000US-0225452P.  
XX 14-AUG-2000; 2000US-0225453P.  
XX 14-AUG-2000; 2000US-0225454P.  
XX 14-AUG-2000; 2000US-0225455P.  
XX 14-AUG-2000; 2000US-0225456P.  
XX 14-AUG-2000; 2000US-0225457P.  
XX 14-AUG-2000; 2000US-0225458P.  
XX 14-AUG-2000; 2000US-0225459P.  
XX 14-AUG-2000; 2000US-0225460P.  
XX 14-AUG-2000; 2000US-0225461P.  
XX 14-AUG-2000; 2000US-0225462P.  
XX 14-AUG-2000; 2000US-0225463P.  
XX 14-AUG-2000; 2000US-0225464P.  
XX 14-AUG-2000; 2000US-0225465P.  
XX 14-AUG-2000; 2000US-0225466P.  
XX 14-AUG-2000; 2000US-0225467P.  
XX 14-AUG-2000; 2000US-0225468P.  
XX 14-AUG-2000; 2000US-0225469P.  
XX 14-AUG-2000; 2000US-0225470P.  
XX 14-AUG-2000; 2000US-0225471P.  
XX 14-AUG-2000; 2000US-0225472P.  
XX 14-AUG-2000; 2000US-0225473P.  
XX 14-AUG-2000; 2000US-0225474P.  
XX 14-AUG-2000; 2000US-0225475P.  
XX 14-AUG-2000; 2000US-0225476P.  
XX 14-AUG-2000; 2000US-0225477P.  
XX 14-AUG-2000; 2000US-0225478P.  
XX 14-AUG-2000; 2000US-0225479P.  
XX 14-AUG-2000; 2000US-0225480P.  
XX 14-AUG-2000; 2000US-0225481P.  
XX 14-AUG-2000; 2000US-0225482P.  
XX 14-AUG-2000; 2000US-0225483P.  
XX 14-AUG-2000; 2000US-0225484P.  
XX 14-AUG-2000; 2000US-0225485P.  
XX 14-AUG-2000; 2000US-0225486P.  
XX 14-AUG-2000; 2000US-0225487P.  
XX 14-AUG-2000; 2000US-0225488P.  
XX 14-AUG-2000; 2000US-0225489P.  
XX 14-AUG-2000; 2000US-0225490P.  
XX 14-AUG-2000; 2000US-0225491P.  
XX 14-AUG-2000; 2000US-0225492P.  
XX 14-AUG-2000; 2000US-0225493P.  
XX 14-AUG-2000; 2000US-0225494P.  
XX 14-AUG-2000; 2000US-0225495P.  
XX 14-AUG-2000; 2000US-0225496P.  
XX 14-AUG-2000; 2000US-0225497P.  
XX 14-AUG-2000; 2000US-0225498P.  
XX 14-AUG-2000; 2000US-0225499P.  
XX 14-AUG-2000; 2000US-0225500P.  
XX 14-AUG-2000; 2000US-0225501P.  
XX 14-AUG-2000; 2000US-0225502P.  
XX 14-AUG-2000; 2000US-0225503P.  
XX 14-AUG-2000; 2000US-0225504P.  
XX 14-AUG-2000; 2000US-0225505P.  
XX 14-AUG-2000; 2000US-0225506P.  
XX 14-AUG-2000; 2000US-0225507P.  
XX 14-AUG-2000; 2000US-0225508P.  
XX 14-AUG-2000; 2000US-0225509P.  
XX 14-AUG-2000; 2000US-0225510P.  
XX 14-AUG-2000; 2000US-0225511P.  
XX 14-AUG-2000; 2000US-0225512P.  
XX 14-AUG-2000; 2000US-0225513P.  
XX 14-AUG-2000; 2000US-0225514P.  
XX 14-AUG-2000; 2000US-0225515P.  
XX 14-AUG-2000; 2000US-0225516P.  
XX 14-AUG-2000; 2000US-0225517P.  
XX 14-AUG-2000; 2000US-0225518P.  
XX 14-AUG-2000; 2000US-0225519P.  
XX 14-AUG-2000; 2000US-0225520P.  
XX 14-AUG-2000; 2000US-0225521P.  
XX 14-AUG-2000; 2000US-0225522P.  
XX 14-AUG-2000; 2000US-0225523P.  
XX 14-AUG-2000; 2000US-0225524P.  
XX 14-AUG-2000; 2000US-0225525P.  
XX 14-AUG-2000; 2000US-0225526P.  
XX 14-AUG-2000; 2000US-0225527P.  
XX 14-AUG-2000; 2000US-0225528P.  
XX 14-AUG-2000; 2000US-0225529P.  
XX 14-AUG-2000; 2000US-0225530P.  
XX 14-AUG-2000; 2000US-0225531P.  
XX 14-AUG-2000; 2000US-0225532P.  
XX 14-AUG-2000; 2000US-0225533P.  
XX 14-AUG-2000; 2000US-0225534P.  
XX 14-AUG-2000; 2000US-0225535P.  
XX 14-AUG-2000; 2000US-0225536P.  
XX 14-AUG-2000; 2000US-0225537P.  
XX 14-AUG-2000; 2000US-0225538P.  
XX 14-AUG-2000; 2000US-0225539P.  
XX 14-AUG-2000; 2000US-0225540P.  
XX 14-AUG-2000; 2000US-0225541P.  
XX 14-AUG-2000; 2000US-0225542P.  
XX 14-AUG-2000; 2000US-0225543P.  
XX 14-AUG-2000; 2000US-0225544P.  
XX 14-AUG-2000; 2000US-0225545P.  
XX 14-AUG-2000; 2000US-0225546P.  
XX 14-AUG-2000; 2000US-0225547P.  
XX 14-AUG-2000; 2000US-0225548P.  
XX 14-AUG-2000; 2000US-0225549P.  
XX 14-AUG-2000; 2000US-0225550P.  
XX 14-AUG-2000; 2000US-0225551P.  
XX 14-AUG-2000; 2000US-0225552P.  
XX 14-AUG-2000; 2000US-0225553P.  
XX 14-AUG-2000; 2000US-0225554P.  
XX 14-AUG-2000; 2000US-0225555P.  
XX 14-AUG-2000; 2000US-0225556P.  
XX 14-AUG-2000; 2000US-0225557P.  
XX 14-AUG-2000; 2000US-0225558P.  
XX 14-AUG-2000; 2000US-0225559P.  
XX 14-AUG-2000; 2000US-0225560P.  
XX 14-AUG-2000; 2000US-0225561P.  
XX 14-AUG-2000; 2000US-0225562P.  
XX 14-AUG-2000; 2000US-0225563P.  
XX 14-AUG-2000; 2000US-0225564P.  
XX 14-AUG-2000; 2000US-0225565P.  
XX 14-AUG-2000; 2000US-0225566P.  
XX 14-AUG-2000; 2000US-0225567P.  
XX 14-AUG-2000; 2000US-0225568P.  
XX 14-AUG-2000; 2000US-0225569P.  
XX 14-AUG-2000; 2000US-0225570P.  
XX 14-AUG-2000; 2000US-0225571P.  
XX 14-AUG-2000; 2000US-0225572P.  
XX 14-AUG-2000; 2000US-0225573P.  
XX 14-AUG-2000; 2000US-0225574P.  
XX 14-AUG-2000; 2000US-0225575P.  
XX 14-AUG-2000; 2000US-0225576P.  
XX 14-AUG-2000; 2000US-0225577P.  
XX 14-AUG-2000; 2000US-0225578P.  
XX 14-AUG-2000; 2000US-0225579P.  
XX 14-AUG-2000; 2000US-0225580P.  
XX 14-AUG-2000; 2000US-0225581P.  
XX 14-AUG-2000; 2000US-0225582P.  
XX 14-AUG-2000; 2000US-0225583P.  
XX 14-AUG-2000; 2000US-0225584P.  
XX 14-AUG-2000; 2000US-0225585P.  
XX 14-AUG-2000; 2000US-0225586P.  
XX 14-AUG-2000; 2000US-0225587P.  
XX 14-AUG-2000; 2000US-0225588P.  
XX 14-AUG-2000; 2000US-0225589P.  
XX 14-AUG-2000; 2000US-0225590P.  
XX 14-AUG-2000; 2000US-0225591P.  
XX 14-AUG-2000; 2000US-0225592P.  
XX 14-AUG-2000; 2000US-0225593P.  
XX 14-AUG-2000; 2000US-0225594P.  
XX 14-AUG-2000; 2000US-0225595P.  
XX 14-AUG-2000; 2000US-0225596P.  
XX 14-AUG-2000; 2000US-0225597P.  
XX 14-AUG-2000; 2000US-0225598P.  
XX 14-AUG-2000; 2000US-0225599P.  
XX 14-AUG-2000; 2000US-0225600P.  
XX 14-AUG-2000; 2000US-0225601P.  
XX 14-AUG-2000; 2000US-0225602P.  
XX 14-AUG-2000; 2000US-0225603P.  
XX 14-AUG-2000; 2000US-0225604P.  
XX 14-AUG-2000; 2000US-0225605P.  
XX 14-AUG-2000; 2000US-0225606P.  
XX 14-AUG-2000; 2000US-0225607P.  
XX 14-AUG-2000; 2000US-0225608P.  
XX 14-AUG-2000; 2000US-0225609P.  
XX 14-AUG-2000; 2000US-0225610P.  
XX 14-AUG-2000; 2000US-0225611P.  
XX 14-AUG-2000; 2000US-0225612P.



PR	02-OCT-2000	2000US-02366032P	
PR	02-OCT-2000	2000US-02370387P	
PR	02-OCT-2000	2000US-02370387P	
PR	02-OCT-2000	2000US-02370393P	
PR	02-OCT-2000	2000US-02370400P	
PR	13-OCT-2000	2000US-02399335P	
PR	13-OCT-2000	2000US-02399337P	
PR	13-OCT-2000	2000US-02403600P	
PR	20-OCT-2000	2000US-02411211P	
PR	20-OCT-2000	2000US-02411856P	
PR	20-OCT-2000	2000US-02417876P	
PR	20-OCT-2000	2000US-02418787P	
PR	20-OCT-2000	2000US-02418088P	
PR	20-OCT-2000	2000US-02418099P	
PR	20-OCT-2000	2000US-02418266P	
PR	01-NOV-2000	2000US-02446177P	
PR	01-NOV-2000	2000US-02466474P	
PR	08-NOV-2000	2000US-02464755P	
PR	08-NOV-2000	2000US-02464767P	
PR	08-NOV-2000	2000US-02464776P	
PR	08-NOV-2000	2000US-02465228P	
PR	08-NOV-2000	2000US-02465233P	
PR	08-NOV-2000	2000US-02465238P	
PR	08-NOV-2000	2000US-02465242P	
PR	08-NOV-2000	2000US-02465256P	
PR	08-NOV-2000	2000US-02465266P	
PR	08-NOV-2000	2000US-02465272P	
PR	08-NOV-2000	2000US-02465288P	
PR	08-NOV-2000	2000US-02466113P	
PR	08-NOV-2000	2000US-02466113P	
PR	08-NOV-2000	2000US-02466113P	
PR	17-NOV-2000	2000US-02492077P	
PR	17-NOV-2000	2000US-02492088P	
PR	17-NOV-2000	2000US-02492099P	
PR	17-NOV-2000	2000US-02492110P	
PR	17-NOV-2000	2000US-02492111P	
PR	17-NOV-2000	2000US-02492123P	
PR	17-NOV-2000	2000US-02492131P	
PR	17-NOV-2000	2000US-02492145P	
PR	17-NOV-2000	2000US-02492156P	
PR	17-NOV-2000	2000US-02492166P	
PR	17-NOV-2000	2000US-02492178P	
PR	17-NOV-2000	2000US-02492188P	
PR	17-NOV-2000	2000US-02492424P	
PR	17-NOV-2000	2000US-02492454P	
PR	17-NOV-2000	2000US-02492464P	
PR	17-NOV-2000	2000US-02492475P	
PR	17-NOV-2000	2000US-02492497P	
PR	17-NOV-2000	2000US-02492529P	
PR	17-NOV-2000	2000US-02493009P	
PR	01-DEC-2000	2000US-02501600P	
PR	01-DEC-2000	2000US-02501603P	
PR	01-DEC-2000	2000US-02501610P	
PR	05-DEC-2000	2000US-02519888P	
PR	05-DEC-2000	2000US-02519893P	
PR	06-DEC-2000	2000US-02514799P	
PR	06-DEC-2000	2000US-02514866P	
PR	06-DEC-2000	2000US-02514868P	
PR	06-DEC-2000	2000US-02514868P	
PR	08-DEC-2000	2000US-02518699P	
PR	08-DEC-2000	2000US-02518699P	
PR	08-DEC-2000	2000US-02519970P	
PR	11-DEC-2000	2000US-02540978P	
PR	05-JAN-2001	2001US-02596788P	
PR	17-JAN-2001	2001US-00764870P	
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Roean CA,	Ruben SM,	Barash SC
XX			
DR	WPI; 2003-743765/70.		
DR	N-PSDB; ADC10754.		
XX			

PT	New isolated nucleic acids and polypeptides, useful for diagnosing,
PT	treating, and/or preventing disorders, such as cancer, infections,
PT	cardiovascular and inflammatory diseases.
XX	
XX	
PS	Claim 11; SEQ ID NO 487; 235bp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (cDNA)
CC	encoding a human extracellular matrix protein, representing one of 161
CC	novel genes. Also included are recombinant vectors, host cells
CC	(expressing the protein), the extracellular matrix proteins (including
CC	their fragments, epitopes and homologues), an isolated antibody that
CC	binds specifically to the protein, diagnosing a pathological condition or
CC	susceptibility to a pathological condition (comprising determining the
CC	presence or absence of a mutation in the nucleic acid and diagnosing a
CC	condition based on the presence or absence of the mutation), diagnosing a
CC	pathological condition or susceptibility to a pathological condition
CC	(comprising determining the presence or amount of expression of the
CC	protein in a biological sample and diagnosing a condition based on the
CC	presence or amount of expression of the protein), preventing, treating or
CC	ameliorating a medical condition by administering the nucleic acid or
CC	protein to a mammalian subject, identifying a binding partner to the
CC	protein, the gene corresponding to the cDNA sequence, and identifying an
CC	activity in a biological assay (comprising expressing the nucleic acid in
CC	a cell, isolating the supernatant, detecting an activity in a biological
CC	assay and identifying the protein in the supernatant having the
CC	activity). The nucleic acids and proteins display the following
CC	activities: Cytostatic, antibacterial, Virucide, Neuroprotective,
CC	Gynaecologic, Gastrointestinal-Gen, Cardiant, Cardiovascular-Gen,
CC	Neurotropic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,
Query Match	16.1%; Score 165; DB 7; Length 189;
Best Local Similarity	28.8%; Pred. No. 1,2e-08;
Matches	36; Conservative 24; Mismatches 53; Indels 12; Gaps 5
Qy	69 CASCS-CPDRMKKGNHCYFSEVBEKDNSSLEFCLADSHLVITDQEMSILQVPLS 1277
Db	68 CLKCAPCPEDMLYLGRKCYFFSEBPRDMNTGRQYCHTHEAVLAVIQSKLEPMFKF-T 126
Qy	128 EAFWIGLGRN-NSGMRWEDSGPLNFSRISSNSFV---QTCAINKNGIQASSCEVPLHG 182
Db	127 REEPIGLRRVDEDFHWVNGDPSFD----PDFTIAGPGCEVFEPTRLVSTECIMTRPW 181
Qy	183 VCKKV 187
Db	182 VCSKM 186
RESULT 14	
AAW78675	
ID	AAW78675 standard; protein; 188 AA.
XX	
AC	AAW78675;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human protein SEQ ID NO 1337.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorder; arthritis; inflammation.
XX	
OS	Homo sapiens.
XX	
PN	WO200157190-A2.
XX	
XX	09-AUG-2001.
XX	
PF	05-FEB-2001; 2001WO-US004098.
XX	
XX	03-FEB-2000; 2000US-00496914.
PR	27-APR-2000; 2000US-00560875.
PR	20-JUN-2000; 2000US-00598075.



Tue Jan 10 09:41:25 2006

us-09-811-367b-1.rag

Page 13

Search completed: January 9, 2006, 15:30:24  
Job time : 90.977 secs

---

This Page Blank



APPLICANT: Hayden-Lebetter, Martha S.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069, 401C1  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 196  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-207-655-196

Query Match 98.4%; Score 1007; DB 4; Length 189;  
Best Local Similarity 98.4%; Pred. No. 2,5e-92;  
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60  
DB 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60  
QY 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
DB 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
QY 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180  
DB 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 181 HGVCCKVRL 189  
DB 181 HGVCCKVRL 189

RESULT 3  
US-10-756-149-5210  
Sequence 5210, Application US/10756149  
Publication No. US20050181375A1  
GENERAL INFORMATION:

APPLICANT: Aziz, Natsasha  
APPLICANT: Zlocznik, Albert  
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
FILE REFERENCE: file  
CURRENT APPLICATION NUMBER: US/10/756,149  
CURRENT FILING DATE: 2004-01-12  
NUMBER OF SEQ ID NOS: 5818  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5210  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-756-149-5210

Query Match 98.4%; Score 1007; DB 5; Length 189;  
Best Local Similarity 98.4%; Pred. No. 2,5e-92;  
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60  
DB 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60  
QY 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
DB 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
QY 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180  
DB 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180  
QY 181 HGVCCKVRL 189  
DB 181 HGVCCKVRL 189

RESULT 4  
US-09-811-367B-3  
Sequence 3, Application US/09811367B  
Patent No. US20020155110A1  
GENERAL INFORMATION:

APPLICANT: GEMINI SCIENCE, INC.  
APPLICANT: Takahashi, No. US20020155110A1uak1  
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)  
FILE REFERENCE: 021286/0278719  
CURRENT APPLICATION NUMBER: US/09/811,367B  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/190,716  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-811-367B-3

Query Match 53.6%; Score 548.5; DB 3; Length 188;  
Best Local Similarity 55.6%; Pred. No. 1.7e-46;  
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60  
DB 1 MADSSIVSTLELPEAPQVQDESRLWKALRPHLSRPAMVALGLITVILMSLWYQRL 60  
QY 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
DB 61 CGGSNYSTCASCPCSDRMKYGNCYFVSVEKQWNSLFECLARDSHLVTITNOEMS 120  
QY 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180  
DB 121 LLQVFLSEAFWCWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 181 HGVCCKV 187  
DB 180 QWICKV 186

RESULT 5  
US-09-811-367B-5  
Sequence 5, Application US/09811367B  
Patent No. US20020155110A1  
GENERAL INFORMATION:

APPLICANT: Takahashi, No. US20020155110A1uak1  
APPLICANT: Mikayama, Toshitumi  
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)  
FILE REFERENCE: 021286/0278719  
CURRENT APPLICATION NUMBER: US/09/811,367B  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/190,716  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 3; Length 188;  
Best Local Similarity 53.5%; Pred. No. 3.4e-44;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;





Db 6 IISLIIIVVAKVGMFLFLLYFPQIQNKNDGFTTTRSYGVISOIFSSSSPENGFIITR 65

Qy 75 -----CPDRWMKYGNHCYFYFSVEKQMNSSLFCLARDSHLLVITDQEMSLQVFLSEA 129

Db 66 SYGVGCPKDEYFQARCFPLSTSESSMNESRDFCKGKSTALIVNTPKFLFDIDDAE 125

Qy 130 FCMVIGL---RNSGMRKEDGSPINFRISNSFPVOTCGAIN-KAGLQASCEVPDHAQVCK 185

Db 126 KYFGLIYHREKRRMRWNNNSVFN-GNVYNNQNFNCATIGLTFTDPAASCDISYRRICE 184

Qy 186 K 186

Db 185 K 185

```

RESULT 9
US-10-741-790-83
; Sequence 83, Application US/10741790
; Publication No. US2004012396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCauley, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-790-83

Query Match      15.5%; Score 159; DB 4; Length 188;
Best Local Similarity 26.5%; Pred. No. 1,4e-07;
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;

41  ITLGLINLVLSV-----LYQWILCOGSN-----YSTC-----ASCPS-----74
6  ITSLIVVIVKVMQMTLFLYFQGIFFKSKNDGFTTTSYGVGQIFSSSPSPNGPIYTR 65

```

```

QY 75 -----CPBRMKYGNHCYFSEVEEKDNSSLFCUARDSHLVITTONQESMLQVFLSEA 129
DB 66 SYGTVCPEKDMFEYQARCFPLSTSEBSWMSRBCFKGKGTLLAVNTPETKFKQIDITDAE 125
QY 130 FCMIGL----RNNSGWRMBEGSPINFSRISNSFVOTCGALIN-KNGIQASSCEVPLHGVCK 185
DB 126 KYFGLIYHREBKRRWRINNSVFN-GNVNQNQNFNCATIGLTPTDPAASCDISYRICE 184
QY 186 K 186
DB 185 K 185

```

```

RESULT 10
US-10-287-436A-69
/ Sequence 69, Application US/10287436A
/ Publication No. US20050202421A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
/ TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
/ TITLE OF INVENTION: RHEUMATOID ARTHRITIS
/ FILE REFERENCE: 10872.514696
/ CURRENT APPLICATION NUMBER: US/10/287,436A
/ CURRENT FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/336,220
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 1446
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 69
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-436A-69

```

	Query Match	15.5%	Score 159;	DB 5;	Length 188;
	Best Local Similarity	26.5%;	Pred. No. 1.4e-07;		
	Matches	48;	Conservative	23;	Mismatches 74; Indels 36; Gaps 7
QY	41 ITLGLTAVLLSV-----LLYOMILCOGSN-----YSTC-----ASCPG-----	74			
Db	6 IISGIIVVLLKVGWTLFLLYFPOLFNKSNDOGFTRSYGVTSQIFGSSSPSPNGFITRR	65			
QY	75 -----CPPRMMKYGNHCYYFSVEEKDNMSSLFPCLARSHLVITDNDMSLIQVPLSEA	129			
Db	66 SYGVTCPEDMFEYQAACEFLTSTSSSMNESRDFCGKSGSTAIVTPPKLFLODITDAE	125			
QY	130 FCMIGL---RNNSGRMEDGSPLNFSRISSNSFYOTCAIN-KNLQASSCEVPPLHGYCK	185			
Db	126 KYFIGLIYHRREKKMRWNINSVFN-GVNTNQNONPNCATIGLTTFPDAAACDISYRICE	184			
QY	186 K 186				
Db	185 K 185				

```

RESULT 11
US-10-287-436A-1251
; Sequence 1251, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1251
; LENGTH: 188

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1251

Query Match      15.5%; Score 159; DB 5; Length 188;
Best Local Similarity 26.5%; Pred. No. 1,4e-07;
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;

QY 41 ITLGLTAVLVS-----LLYQWILCGSN-----YSTC-----ASCPS----- 74
DB 6 ITSGILVVLKVGKMTLFLIPQIPKNSDGETTRTSVGTYSQIRGSSSPSPNGFITTR 65
QY 75 -----CPDRMKXGNHCYFVSVEKWNSSLEFCIARDSHLVTITDQEMSLIQVFLSEA 129
DB 66 SYGTVCFKDMEFYQARCFILSTSESSWNESRDPCKGKSTLAIVNTPEKIKFLQDITDAE 125
QY 130 FCHIGL---RNSGMRWEDGSPINFRISNSFVOTCGAI-N-KNGIQASSCEVPFLHGVCK 185
DB 126 KYFIIGLIYHREKRWKRWINSVFN-GAVTINQONFNCATIGLTKTIDPASCDSYRRIE 184
QY 186 K 186
DB 185 K 185

RESULT 12
US-11-097-143-5490
; Sequence 5490, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,932
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5490
; LENGTH: 188
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-5490

Query Match      10.1%; Score 103.5; DB 6; Length 188;
Best Local Similarity 21.0%; Pred. No. 0.051;
Matches 39; Conservative 26; Mismatches 66; Indels 55; Gaps 9;

QY 49 VLISVLVYOWILC-----QGSNYSTGASCPC-----PDRW-----MKYGNHCYF 89
DB 5 LILSVIISLQGLCLLDRTMATPPKPGPVADCPNCVDSQYTPMKMTMPLIKLGEKRYYL 64
QY 90 SVEEK-DWNSLEFCIARDSHLVTITDQEMSLIQVFLSEAFCHIGLRNNSGW----- 141
DB 65 GIPFKAMFKATQYCRVYHGMILASISQGEENDRLKHIRD---FGIGHEHFWISGTDLA 120

```

```

QY 142 -----RWEDGSPINFRISNSFVOTCGAI-NKNG-----LQASSCEVP 179
DB 121 DEGNFEMATGRPIFTYMNAGEPNFR--YENGEEENCLIELNRDQKGLKWNDSFCSPE 178
QY 180 LHGVCK 185
DB 179 TYFVCE 184

RESULT 13
US-10-114-893-48
; Sequence 48, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Treacy, Maurice
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-48

Query Match      9.8%; Score 100.5; DB 4; Length 189;
Best Local Similarity 37.3%; Pred. No. 0.1;
Matches 19; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 70 ASCPS-CPDRMKXGNHCYFVSVEKWNSSLEFCIARDSHLVTITDQEM 119
DB 138 ANCSAPCPQDMWHGENCYLFFSGSFNWEKSGEKCLSDAKLIKINSTADL 188

RESULT 14
US-10-369-493-5642
; Sequence 5642, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5642
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5642

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.7044 Seconds  
(without alignments)  
149.966 Million cell updates/sec

Title: US-09-811-367b-1  
Perfect score: 1023  
Sequence: 1 MTDSVYISMLEPLPTAQAQN.....GLQASSCEVPLHGCKKQVRL 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues  
Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/PCR\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US05\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	100.0	189	6	US-10-055-877-209 Sequence 209, App
2	1007	98.4	189	6	US-10-055-877-207 Sequence 207, App
3	548.5	53.6	188	6	US-10-055-877-205 Sequence 205, App
4	525.5	51.4	188	6	US-10-055-877-206 Sequence 206, App
5	47	4.6	189	7	US-11-147-492-30 Sequence 30, Appl
6	44	4.3	189	6	US-10-821-234-1432 Sequence 1432, App
7	44	4.3	189	6	US-10-878-556A-193 Sequence 193, App
8	42.5	4.2	188	6	US-10-980-388-90 Sequence 90, Appl
9	41.5	4.1	189	7	US-11-147-492-10 Sequence 10, Appl
10	41.5	4.1	189	7	US-11-147-492-20 Sequence 20, Appl
11	41	4.0	189	7	US-11-137-465-60 Sequence 60, Appl
12	40.5	4.0	189	7	US-11-147-492-28 Sequence 28, Appl
13	38.5	3.8	189	7	US-11-147-492-24 Sequence 24, Appl
14	38	3.7	188	6	US-10-467-657-2750 Sequence 2750, App
15	38	3.7	189	6	US-10-467-657-2750 Sequence 806, App
16	36.5	3.6	189	7	US-11-147-492-16 Sequence 16, Appl
17	35.5	3.5	188	6	US-10-945-853-1 Sequence 1, Appl
18	35.5	3.5	189	6	US-10-467-657-6250 Sequence 6250, App
19	35	3.4	189	6	US-10-821-234-1421 Sequence 1421, App
20	35	3.4	189	7	US-11-205-109-33 Sequence 33, Appl
21	34.5	3.4	188	6	US-10-884-730-88 Sequence 88, Appl
22	34.5	3.4	188	6	US-10-945-853-2 Sequence 2, Appl
23	33	3.2	188	7	US-11-064-774A-117 Sequence 117, App
24	33	3.2	189	6	US-10-131-826A-240 Sequence 240, App
25	33	3.2	189	6	US-10-467-657-3184 Sequence 3184, App

26	33	3.2	189	7	US-11-147-492-26 Sequence 26, Appl
27	32.5	3.2	188	6	US-10-980-388-101 Sequence 101, App
28	32.5	3.2	189	7	US-11-147-492-12 Sequence 12, Appl
29	32	3.1	188	7	US-11-055-822-152 Sequence 152, App
30	31.5	3.1	188	6	US-10-467-657-4044 Sequence 4044, App
31	31	3.0	188	6	US-10-467-657-920 Sequence 920, App
32	31	3.0	188	7	US-11-000-463-866 Sequence 866, App
33	31	3.0	188	7	US-11-000-463-867 Sequence 867, App
34	31	3.0	189	6	US-10-467-657-4692 Sequence 4692, App
35	31	3.0	189	7	US-11-071-262-1 Sequence 1, Appl
36	31	3.0	189	7	US-11-147-492-6 Sequence 6, Appl
37	31	3.0	189	7	US-11-147-492-22 Sequence 22, Appl
38	30.5	3.0	188	6	US-10-842-206-40 Sequence 40, Appl
39	30.5	3.0	188	6	US-10-980-459-32 Sequence 32, Appl
40	30.5	3.0	188	7	US-11-147-492-8 Sequence 8, Appl
41	30	2.9	188	6	US-10-131-826A-2 Sequence 2, Appl
42	30	2.9	188	6	US-10-793-626-152 Sequence 152, App
43	30	2.9	188	6	US-10-821-234-1316 Sequence 1316, App
44	30	2.9	188	7	US-11-054-515-3235 Sequence 3235, App
45	30	2.9	188	7	US-11-194-246-292 Sequence 292, App

ALIGNMENTS

RESULT 1  
US-10-055-877-209  
Sequence 209, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: Decristofaro, Marc  
APPLICANT: Padisaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Veltzar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytek, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Rekuda, Ramesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patuturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Bisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055.877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262.992  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263.598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263.799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264.117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264.139  
PRIOR FILING DATE: 2001-01-25

```

; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 209
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-209

Query Match          100.0%; Score 1023; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLTAVLSVLLYQWIL 60
DB 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLTAVLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPSPDRMKYGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQMS 120
DB 61 CQGSNYSTCASCPSPDRMKYGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQMS 120
QY 121 LLQVFLSEAFPCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
DB 121 LLQVFLSEAFPCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 2
US-10-055-877-207
; Sequence 207, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigarlu, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Raccelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eising, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verne, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
```

```

; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 207
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-207

Query Match          98.4%; Score 1007; DB 6; Length 189;
Best Local Similarity 98.4%; Pred. No. 2.5e-98;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLTAVLSVLLYQWIL 60
DB 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLTAVLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPSPDRMKYGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQMS 120
DB 61 CQGSNYSTCASCPSPDRMKYGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQMS 120
QY 121 LLQVFLSEAFPCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
DB 121 LLQVFLSEAFPCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 3
US-10-055-877-205
; Sequence 205, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigarlu, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Raccelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
```

```

; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT:
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 205
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-055-877-205

Query Match      53.6%; Score 548.5; DB 6; Length 188;
Best Local Similarity 55.6%; Pred. No. 1.8e-50;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY      1 MTDVSYSMLELPATQAQNDYGPQKSSSKSCGLVATTGLTFLAVLISVLYQMIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MADSSIVSTLELPAPAPVQDESRRWKLKAVLHRRPHLSFPAWVALGLTVIILMSLTYRIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 CQGSNVTCTASCPCSPRMMKYGNGHCYFVSVEKDNMSLSEFCIARDSHLLVITDNOEMS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 CCGSKDSTCTCHPCPCPLMTWTNGSHCYFSEMEKDNMSLSEFCADKSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      121 LLAQVFLSEAFCMWGLRNNSGWRWEDGSPINFSRISNSPVOTCGAINKNGIQASSCEVPL 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 LFGSYILOQDPFYWIGLRNIDGWRWEGGPAISL-RILTNSLIGRCAGIHRNGIQASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      181 HGVCCKV 187
      :||||
Db      180 QWICKV 186
      :||||

RESULT 4
US-10-055-877-206
; Sequence 206, Application US/10055877
```

```

; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT:
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 206
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-055-877-206

Query Match      51.4%; Score 525.5; DB 6; Length 188;
Best Local Similarity 53.5%; Pred. No. 4.6e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY      1 MTDVSYSMLELPATQAQNDYGPQKSSSKSCGLVATTGLTFLAVLISVLYQMIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MADNSIVSTLELPAPAPVQDSDRWKVKAVLHRRPVSLVWVALGLTVIILMSLTYRIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 CQGSNVTCTASCPCSPRMMKYGNGHCYFVSVEKDNMSLSEFCIARDSHLLVITDNOEMS 120
```

```

Db      61 CCGSKGFMCSQCRCPLMWRNGSHCYFSMEKRDONSLSKFCADKGSHTLTFPPNOGVN 120
QY      121 LLOVFLSEAFQWIGIRNNSGWRWEDGSPINFRISNSVVOCGALINKGLOASSCEVPL 180
Db      121 LFOEVGDEFWIGLKDIDGWRWEDGDPALSLSLSNSVVOCGTHRCGLHASSCEVAL 179
QY      181 HGVCKV 187
Db      180 CMICKV 186

```

```

RESULT 5
US-11-147-492-30
; Sequence 30, Application US/11147492
; Publication No. US20050276785A1
; GENERAL INFORMATION:
; APPLICANT: Kapp, Joachim-Freidrich
; APPLICANT: Kuehl, Uwe
; APPLICANT: Groetzsch, Georg
; APPLICANT: Schultheiss, Heinz-Peter
; APPLICANT: Schwede, Olaf
; APPLICANT: Stuerzebecher, Claus-Steffen
; TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
; FILE REFERENCE: 53223
; CURRENT APPLICATION NUMBER: US/11/147,492
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 189
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-147-492-30

```

```

Query Match      4.6%; Score 47; DB 7; Length 189;
Best Local Similarity 24.2%; Pred. No. 4.3e+02;
Matches 40; Conservative 20; Mismatches 57; Indels 48; Gaps 10;

QY      39 VAITGLTAVLLSVLLYQWILCOGSNSTCASC-----SC-PDRWM 80
Db      1 MALSTSLMAVL--VLSTYKICSLGCDLPQTHSLGNRRALILAQGRISPSCUKDR-- 56
QY      81 KGNHCYYSVEKKNSSLEFCLARDSHLVITTNQESLLOVFLSEAFQWIGIRNNSG 140
Db      57 ---HDFGPQEEFGN---QFOKA-----QALSVLHEMIQOTFNLFTKDS 98
QY      141 WRWEDGSPINFRISNSF--VOTCGAINKGLOASSCEVPLHGV 183
Db      99 -TWEGSLEKFTSLNQQLNDMEAC-VIOEGVE---ETPLMNV 137

```

```

RESULT 6
US-10-821-234-1432
; Sequence 1432, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1432
; LENGTH: 189

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1432

```

```

Query Match      4.3%; Score 44; DB 6; Length 189;
Best Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

```

```

QY      7 YSMLEPPTATQANDYGPQKSSSS-----KPSCSCLVAITGLTAVLLSVLLYQW 58
Db      67 YDVVLP-----GNIUGQNISESAAVKEILKEQENRKGLIATCAGPALAHRIGF-- 119
QY      59 ILCOGSNSTCASCSPDRMKYGNHCYYSVEKDW-----NSSLFCLA 105
Db      120 ---GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTFEPALA 167

```

```

RESULT 7
US-10-878-556A-193
; Sequence 193, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: humanap/chrl-014805
; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-193

```

```

Query Match      4.3%; Score 44; DB 6; Length 189;
Best Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

```

```

QY      7 YSMLEPPTATQANDYGPQKSSSS-----KPSCSCLVAITGLTAVLLSVLLYQW 58
Db      67 YDVVLP-----GNIUGQNISESAAVKEILKEQENRKGLIATCAGPALAHRIGF-- 119
QY      59 ILCOGSNSTCASCSPDRMKYGNHCYYSVEKDW-----NSSLFCLA 105
Db      120 ---GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTFEPALA 167

```

```

RESULT 8
US-10-980-388-90
; Sequence 90, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325_US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304

```



```
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,303
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,397
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,247
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/188,880
/ PRIOR FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: 60/217,369
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/217,370
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/218,492
/ PRIOR FILING DATE: 2000-07-20
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 90
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-980-388-90

Query Match
Best Local Similarity 4.1%; Score 42.5; DB 6; Length 188;
Matches 24; Conservative 15; Mismatches 36; Indels 35; Gaps 6;

QY 64 SNVSTCASC-----SCPRMKNKYG---NHCIYFVSEKDMNSLSLEFCLARDSHLVTITDNG 117
DB 26 SQSCKTQPLDNLGNCLDYLFGKTKTNLYF-----TTTFSLHESYSLEI---Q 72
QY 118 EMSLQVFLSEAFPCWIGLRNNSGWRWEDGSPLNFSRISNSFYOTCGAIN 167
DB 73 LFPKLTLEMSPF-----SGRP--FPLVEDSFGQRCQGN 106

RESULT 9
US-11-147-492-10
/ Sequence 10, Application US/11147492
/ Publication No. US20050276785A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapp, Joachim-Freidrich
/ APPLICANT: Kuehl, Uwe
/ APPLICANT: Groetzbach, Georg
/ APPLICANT: Schultheiss, Heinz-Peter
/ APPLICANT: Sowade, Olaf
/ APPLICANT: Stuerzebecher, Claus-Steffen
/ TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
/ FILE REFERENCE: 53223
/ CURRENT APPLICATION NUMBER: US/11/147,492
/ PRIOR FILING DATE: 2005-06-07
/ PRIOR APPLICATION NUMBER: US 60/579,024
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-147-492-10

Query Match
Best Local Similarity 4.1%; Score 41.5; DB 7; Length 189;
Matches 31; Conservative 14; Mismatches 39; Indels 37; Gaps 6;
```

```
QY 130 F 130
DB 113 Y 113

RESULT 10
US-11-147-492-20
/ Sequence 20, Application US/11147492
/ Publication No. US20050276785A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapp, Joachim-Freidrich
/ APPLICANT: Kuehl, Uwe
/ APPLICANT: Groetzbach, Georg
/ APPLICANT: Schultheiss, Heinz-Peter
/ APPLICANT: Sowade, Olaf
/ APPLICANT: Stuerzebecher, Claus-Steffen
/ TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
/ FILE REFERENCE: 53223
/ CURRENT APPLICATION NUMBER: US/11/147,492
/ PRIOR FILING DATE: 2005-06-07
/ PRIOR APPLICATION NUMBER: US 60/579,024
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 20
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-147-492-20

Query Match
Best Local Similarity 4.1%; Score 41.5; DB 7; Length 189;
Matches 31; Conservative 13; Mismatches 40; Indels 37; Gaps 6;

QY 39 VAITGLTFAVLTVLTVLQWITLCOGSNYSTCASC-----SC-PDRM 80
DB 1 MALSFSLMANVL--VLSYKSLCSLGCDDLQPTHSLGNRRALLILQMGRIHSFSLCKDR-- 56
QY 81 KYGNHCYFVSEKDMN-----SLEFCLARDSHLVTITDNG---EMSLQVFLSEA 129
DB 57 ----HDFRIPQEEFDGQFOKAQALSVLHEMIQOTFNLFTEDSSAAMEQSLLKEFSTEL 112
QY 130 F 130
DB 113 Y 113

RESULT 11
US-11-137-465-60
/ Sequence 60, Application US/11137465
/ Publication No. US2005025558A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia, K.
/ APPLICANT: Smith, Randall, F.
/ APPLICANT: Xiang, Zhaoying
/ APPLICANT: Kadnick, Karen
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50018
/ CURRENT APPLICATION NUMBER: US/11/137,465
/ PRIOR FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US/10/239,663
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: PCT/US01/09226
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: 60/192,158
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/192,668
/ PRIOR FILING DATE: 2000-03-27
/ PRIOR APPLICATION NUMBER: 60/200,166
/ PRIOR FILING DATE: 2000-04-27
```

NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 60  
 LENGTH: 189  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-137-465-60

Query Match 4.0%; Score 41; DB 7; Length 189;  
 Best Local Similarity 25.0%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 8; Mismatches 28; Indels 12; Gaps 3;

QY 61 CGGSNYSTCASCPCSPDRMKYGNHCYFSVEKDNSSLFC--LADSHLVTIDNQ 117  
 DB 121 CCG-----TCPALNSLRHSSFEYKRAVPTCP--LFCRCPTMTLFLSLWQDDDH 171

QY 118 EMSL 121  
 DB 172 KMSV 175

RESULT 12

US-11-147-492-28  
 Sequence 28, Application US/11147492  
 Publication No. US2005026785A1

GENERAL INFORMATION:

APPLICANT: Kapp, Joachim-Freidrich  
 APPLICANT: Kuehl, Uwe  
 APPLICANT: Groetzbach, Georg  
 APPLICANT: Schultheiss, Heinz-Peter  
 APPLICANT: Sowade, Olaf  
 APPLICANT: Stuerzebecher, Claus-Steffen  
 TITLE OF INVENTION: Treatment of Cardiomyopathy and Endothelial Dysfunction  
 FILE REFERENCE: 53223  
 CURRENT APPLICATION NUMBER: US/11/147,492  
 CURRENT FILING DATE: 2005-06-07  
 PRIOR APPLICATION NUMBER: US 60/579,024  
 PRIOR FILING DATE: 2004-06-04  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 28  
 LENGTH: 189  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-11-147-492-28

Query Match 4.0%; Score 40.5; DB 7; Length 189;  
 Best Local Similarity 25.6%; Pred. No. 2e+03;  
 Matches 31; Conservative 13; Mismatches 40; Indels 37; Gaps 6;

QY 39 VAITIGLTLAVLSTVLVYMWILCOGSNYSTCASC-----SC-PDRKM 80  
 DB 1 MLSTSLMLAVL--VLSTYKSLGCDLPQTHSLGNRRALLLAQNGRISPPSLKDR-- 56

QY 81 KXGNICYFSVEKDN-----SSLFCLARDSHLVTIDNQ---EMSLQVFLSEA 129  
 DB 57 ----HDFGLPQEFPGDNQOKTOAISVLHEMIGQTFNLFSTEDSSAAMQSILEKFTSL 112

QY 130 F 130  
 DB 113 Y 113

RESULT 13

US-11-147-492-24

Sequence 24, Application US/11147492  
 Publication No. US2005026785A1

GENERAL INFORMATION:

APPLICANT: Kapp, Joachim-Freidrich  
 APPLICANT: Kuehl, Uwe  
 APPLICANT: Groetzbach, Georg  
 APPLICANT: Schultheiss, Heinz-Peter  
 APPLICANT: Sowade, Olaf

APPLICANT: Stuerzebecher, Claus-Steffen  
 TITLE OF INVENTION: Treatment of Cardiomyopathy and Endothelial Dysfunction  
 FILE REFERENCE: 53223  
 CURRENT APPLICATION NUMBER: US/11/147,492  
 CURRENT FILING DATE: 2005-06-07  
 PRIOR APPLICATION NUMBER: US 60/579,024  
 PRIOR FILING DATE: 2004-06-04  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 24  
 LENGTH: 189  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-11-147-492-24

Query Match 3.8%; Score 38.5; DB 7; Length 189;  
 Best Local Similarity 24.6%; Pred. No. 3.2e+03;  
 Matches 15; Conservative 10; Mismatches 21; Indels 15; Gaps 3;

QY 85 HCYFSVEKDNSSLFCLARDSHLVTIDNQEMSLQVFLSEAFQWIGLRNNGMRWE 144  
 DB 57 HDFEPQEFPGDN--QFOKA-----QAISVLHEMIGQTFNLFSTNGSSA--AMD 101

QY 145 D 145  
 DB 102 E 102

RESULT 14

US-10-467-657-2750  
 Sequence 2750, Application US/10467657  
 Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA  
 APPLICANT: FONTANA Maria Rita  
 APPLICANT: PIZZA Mariagrazia  
 APPLICANT: MASIGNANI Vega  
 APPLICANT: MONACI Elisabetta  
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 FILE REFERENCE:  
 CURRENT APPLICATION NUMBER: US/10/467,657  
 CURRENT FILING DATE: 2003-08-11  
 PRIOR APPLICATION NUMBER: GB-0103424.8  
 PRIOR FILING DATE: 2001-02-12  
 NUMBER OF SEQ ID NOS: 9218  
 SOFTWARE: SeqMin99, version 1.04  
 SEQ ID NO: 2750  
 LENGTH: 188  
 TYPE: PRT  
 ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-2750

Query Match 3.7%; Score 38; DB 6; Length 188;  
 Best Local Similarity 20.0%; Pred. No. 3.6e+03;  
 Matches 15; Conservative 14; Mismatches 14; Indels 32; Gaps 3;

QY 4 SVIYEMLETPRATQANQNGYPOQSSSKPSCSLVATIGL-----LTAVLIS 52  
 DB 32 ALIYEMLVGAT-----CLAALLAGIAIPLAVPSIAVSALVTS 71

QY 53 VLLY-QWILCOGSNY 66  
 DB 72 IILMGAMWLYFRANW 86

RESULT 15

US-10-995-561-806  
 Sequence 806, Application US/10995561  
 Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

;  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 806  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-806

Query Match 3.7%; Score 38; DB 6; Length 189;  
Best Local Similarity 35.0%; Pred. No. 3.6e+03;  
Matches 7; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 77 DRMKYGNHCYRFSVEKDW 96  
DB 29 DGMVYYANH---TEEKQW 44

Search completed: January 9, 2006, 15:56:42  
Job time : 11.7044 secs

THE BOOK OF  
JEREMIAH

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 9, 2006, 14:41:26 ; Search time 87.515 Seconds  
(without alignments)  
943.913 Million cell updates/sec

Title: US-09-811-367b-3

Perfect score: 1029  
Sequence: 1 MADSSIVSTLELPAPQVOD.....GLQSSCEVALQMICRKLIV 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 6014

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A\_Geneseq\_21: \*  
2: geneseqp1980a: \*  
3: geneseqp1990a: \*  
4: geneseqp2000a: \*  
5: geneseqp2001a: \*  
6: geneseqp2002a: \*  
7: geneseqp2003a: \*  
8: geneseqp2004a: \*  
9: geneseqp2005a: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	AAE11760	AAE11760 Mouse mas
2	838	81.4	188	AAE11760	AAE11760 Mammalian
3	838	81.4	188	AAE11760	AAE11760 Rat mast
4	838	81.4	188	AAE11760	AAE11760 Rat mast
5	568.5	55.2	189	ADD25635	ADD25635 Binding d
6	568.5	55.2	189	ADD25635	ADD25635 PRO polyP
7	548.5	53.3	189	AAW88265	AAW88265 Human mas
8	548.5	53.3	189	AAE11759	AAE11759 Human mas
9	152.5	15.8	188	AAE11759	AAE11759 Chicken M
10	152	14.8	189	AAU19837	AAU19837 Human nov
11	152	14.8	189	AAU19837	AAU19837 Human nov
12	152	14.8	189	ABP48057	ABP48057 Human pol
13	152	14.8	189	ADCI1019	ADCI1019 Human pro
14	143.5	13.9	188	AAW78675	AAW78675 Human pro
15	143.5	13.9	188	AAU00671	AAU00671 Human INT
16	143.5	13.9	188	ABO32533	ABO32533 Secreted
17	143.5	13.9	188	ADP65310	ADP65310 Human c-t
18	143.5	13.9	188	ADQ10144	ADQ10144 Human pol
19	143.5	13.9	188	ADP25141	ADP25141 PRO polyP
20	88.5	8.6	189	ABE70262	ABE70262 E-selecti
21	83	8.1	188	ABBS5966	ABBS5966 Drosophi
22	72.5	7.0	188	ABBS5966	ABBS5966 Drosophi
23	69.5	6.8	189	ADC38690	ADC38690 Human sec
24	56	5.4	189	ABG30869	ABG30869 P. yoelli

25	55.5	5.4	189	4	ABE5153	ABE5153 Basic fib
26	55	5.3	189	3	AAE56537	AAE56537 Arabidops
27	54.5	5.3	189	2	ABU01363	ABU01363 S. pneumo
28	53.5	5.2	189	6	AAW98509	AAW98509 H. pylori
29	53	5.2	188	6	ABM69571	ABM69571 Phototrab
30	53	5.2	189	7	ADC37367	ADC37367 Nuclear E
31	53	5.2	189	8	ADR58963	ADR58963 Human E1K
32	52.5	5.1	188	3	AAE60348	AAE60348 Arabidops
33	52.5	5.1	188	3	AAE19860	AAE19860 Arabidops
34	52.5	5.1	189	4	ABG07567	ABG07567 Novel hum
35	52	5.1	188	4	AAE91196	AAE91196 C. glutami
36	52	5.1	188	7	ADP06947	ADP06947 Bacterial
37	52	5.1	189	7	ADM04618	ADM04618 Human pro
38	52	5.1	189	8	ADR58961	ADR58961 Human E1K
39	51.5	5.0	188	8	ABG02083	ABG02083 Novel hum
40	51.5	5.0	188	9	ABW93149	ABW93149 M. xanthu
41	51	5.0	189	3	AAE38441	AAE38441 L. pneumo
42	51	5.0	189	9	ABU11464	ABU11464 Human MDD
43	50.5	4.9	189	6	ABE19732	ABE19732 S. coelic
44	50.5	4.9	189	9	AEA48225	AEA48225 Subfamily
45	50.5	4.9	189	9	AEA48225	AEA48225 Subfamily

## ALIGNMENTS

RESULT 1  
AAE11760  
ID AAE11760 standard; protein; 188 AA.

XX AAE11760;

XX DT 18-DEC-2001 (first entry)

XX DE Mouse mast cell function associated antigen (MAFA) protein.

XX KW Mouse; pharmaceutical composition; mast cell function associated antigen;

XX KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;

XX KW immunosuppressive; cytostatic.

XX OS Mus sp.

XX PH Key Location/Qualifiers  
64.188  
/note="Extracellular domain"

XX FT Domain

XX PD WO200170805-A2.

XX PF 27-SEP-2001.

XX PF 16-MAR-2001; 2001WO-US008596.

XX PR 17-MAR-2000; 2000US-0190716P.

XX PA (GEMT-) GEMINI SCI INC.

XX PI Takahashi N, Miyayama T;

XX DR WPI; 2001-611482/70.

XX DR N-PSDB; AAD18735.

XX PT Pharmaceutical composition for treating tumor by stimulating cytotoxic

XX PS activity of natural killer cell or T-cell, comprises an agent that binds

XX CC to mast cell function-associated antigen ligand on target cell.

XX CC Example 1, Page 19; 49pp; English.

XX CC The present invention relates to a pharmaceutical composition comprising

XX CC an agent which specifically binds to a mast cell function associated

XX CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural

XX CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA

XX CC ligand and a pharmaceutically acceptable excipient. The invention is

XX CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA

CC binding to a ligand on a target cell, by contacting the pharmaceutical  
 CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX Sequence 188 AA;

Query Match 100.0%; Score 1029; DB 4; Length 188;

Best Local Similarity 100.0%; Pred. No. 1,1e-102; Indels 0; Gaps 0;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODSRWKLKAVLHRLSPFAMVALGLITVILMSLWYORIL 60  
 DB 1 MADSSYSTLELPEAPQVODSRWKLKAVLHRLSPFAMVALGLITVILMSLWYORIL 60  
 QY 61 CGSGKDSCTSHCPSPILMTNRNGSHCYFSMEKQWNSLKRCAKGSHTLTFPNQGVK 120  
 DB 61 CGSGKDSCTSHCPSPILMTNRNGSHCYFSMEKQWNSLKRCAKGSHTLTFPNQGVK 120  
 QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIORCGAIHRNGLQASCEVALQ 180  
 DB 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIORCGAIHRNGLQASCEVALQ 180  
 QY 181 WICKKVL 188  
 DB 181 WICKKVL 188

## RESULT 2

AA877033  
 ID AAR77033 standard; protein; 188 AA.

AA877033;

01-FEB-1996 (first entry)

Mammalian mast cell function-associated antigen (MAFA).

Mast cell function-associated antigen; MAFA; soluble; ligand;  
 identification; screening; inflammation; inflammatory; allergy; allergic;  
 prevention.

Rattus rattus.

WO9527734-A1.

19-OCT-1995.

06-APR-1995; 95WO-US004258.

08-APR-1994; 94TL-00109257.

(YEDA ) YEDA RES & DEV CO LTD.

(RYCU/) RYCUS A.

Pecht I, Gutmann MD, Tal M;

WPI, 1995-366356/47.

N-PSDB; AAT01471.

Novel DNA encoding a mast cell function-associated antigen (MAFA) -  
 useful for screening for ligands of MAFA which are useful for prevention  
 of inflammatory and allergic reactions.

Claim 12; Page 37; 54pp; English.

A soluble form of mast cell function-associated antigen (MAFA) can be  
 produced by recombinant techniques for use in the ligand- screening

CC assay. The ligands that are identified may be used alone or in  
 CC combination with the MAFA to prevent inflammatory and allergic reactions

XX Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;

Best Local Similarity 80.7%; Pred. No. 5.2e-82; Indels 0; Gaps 0;  
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODSRWKLKAVLHRLSPFAMVALGLITVILMSLWYORIL 60  
 DB 1 MADSSYSTLELPEAPQVODSRWKLKAVLHRLSPFAMVALGLITVILMSLWYORIL 60  
 QY 61 CGSGKDSCTSHCPSPILMTNRNGSHCYFSMEKQWNSLKRCAKGSHTLTFPNQGVK 120  
 DB 61 CGSGKDSCTSHCPSPILMTNRNGSHCYFSMEKQWNSLKRCAKGSHTLTFPNQGVK 120  
 QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIORCGAIHRNGLQASCEVALQ 180  
 DB 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIORCGAIHRNGLQASCEVALQ 180  
 QY 181 WICKKVL 187  
 DB 181 WICKKVL 187

## RESULT 3

AA88277  
 ID AAW88277 standard; protein; 188 AA.

AAW88277;

29-MAR-1999 (first entry)

Rat mast cell function-associated antigen (MAFA).

Mast cell function-associated antigen; MAFA; splice variant; rat;  
 inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

Rattus sp.

WO9854209-A2.

03-DEC-1998.

29-MAY-1998; 98WO-GB001572.

31-MAY-1997; 97GB-00011148.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

WPI, 1999-059806/05.

N-PSDB; AAW84222.

New polypeptide having a sequence corresponding to human mast cell  
 function-associated antigen - useful in forming and manufacturing  
 pharmaceutical compositions in the treatment of inflammatory and allergic  
 diseases, and tumour growth.

Disclosure; Fig 4; 44pp; English.

This is the amino acid sequence of rat mast cell function-associated  
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and  
 CC basophils. The invention relates to cloning of the human MAFA molecule  
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)

CC of human MAFA that are not found in rat. Polypeptides and synthetic  
CC peptides (see AAW8258-64) based on human MAFA and human truncated MAFA,  
CC and polynucleotides encoding them, can be used in methods for the  
CC treatment of inflammatory and allergic diseases (e.g. rheumatoid  
CC arthritis and asthma), and tumour growth

CC Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;

Best Local Similarity 80.7%; Pred. No. 5.2e-82;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODESRMKLKAVLRPHLSRFAMVALGLITVIMSLMYQRL 60  
DB 1 MADNSYSTLELPAAPRVQDDSRMKYKAVLRPCVSYLWVVALGLITVIMSLLYQRTL 60  
QY 61 CCGSKDSTGSHCPSPILMTNRNGSHCYFSMEKDMNSSLKPCADKSHLTFPPNQGVK 120  
DB 61 CCGSKGFMCSQCSRCENLMNRNGSHCYFSMEKRDNSSLKPCADKSHLTFPPNQGVN 120  
QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPPALSLRILTNLSLQRCGAIHRNGLOASSCEVALQ 180  
DB 121 LFGELYGDPFYWIGLRNIDGMRWEDGPALSLSLNSVQKCTIHRGGLHSSCEVALQ 180  
QY 181 WICKKVL 187  
DB 181 WICKKVL 187

RESULT 4

AAE11761 ID AAE11761 standard; protein; 188 AA.

XX AAE11761;

DT 18-DEC-2001 (first entry)

DE Rat mast cell function associated antigen (MAFA) protein.

XX Rat; pharmaceutical composition; mast cell function associated antigen;

KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;

KW immunosuppressive; cytostatic.

XX Rattus norvegicus.

PN WO200170805-A2.

PD 27-SEP-2001.

PF 16-MAR-2001; 2001WO-US008596.

PR 17-MAR-2000; 2000US-0190716P.

PA (GEM1-) GEMINI SCI INC.

PI Takahashi N, Mikayama T;

DR WPI; 2001-611482/70.

XX N-PSDB; AAD18736.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic

XX activity of natural killer cell or T-cell, comprises an agent that binds

XX to mast cell function-associated antigen ligand on target cell.

XX Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising

XX an agent which specifically binds to a mast cell function associated

XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural

XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA

XX ligand and a pharmaceutically acceptable excipient. The invention is

XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA

XX binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition  
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
CC on the target cell. The agent or the composition is useful for treating a  
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
CC tumour cell. The invention is also useful for inhibiting an activity of  
CC NK cell or a T-cell. The present sequence is rat MAFA protein

XX Sequence 188 AA;

Query Match 81.4%; Score 838; DB 4; Length 188;

Best Local Similarity 80.7%; Pred. No. 5.2e-82;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODESRMKLKAVLRPHLSRFAMVALGLITVIMSLMYQRL 60  
DB 1 MADNSYSTLELPAAPRVQDDSRMKYKAVLRPCVSYLWVVALGLITVIMSLLYQRTL 60  
QY 61 CCGSKDSTGSHCPSPILMTNRNGSHCYFSMEKDMNSSLKPCADKSHLTFPPNQGVK 120  
DB 61 CCGSKGFMCSQCSRCENLMNRNGSHCYFSMEKRDNSSLKPCADKSHLTFPPNQGVN 120  
QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPPALSLRILTNLSLQRCGAIHRNGLOASSCEVALQ 180  
DB 121 LFGELYGDPFYWIGLRNIDGMRWEDGPALSLSLNSVQKCTIHRGGLHSSCEVALQ 180  
QY 181 WICKKVL 187  
DB 181 WICKKVL 187

RESULT 5

ADD25635 ID ADD25635 standard; protein; 189 AA.

XX ADD25635;

DT 15-JUN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated protein #95.

XX Binding domain; immunoglobulin; fusion protein; cyostatic;

KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;

KW neuroprotective; hinge region; immunoglobulin heavy chain;

KW CH2 constant region; CH3 constant region; IgG1;

KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;

KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;

KW rheumatoid arthritis; myasthenia gravis; Grave's disease;

KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

PN US2003118592-A1.

PD 25-JUN-2003.

PF 25-JUL-2002; 2002US-00207655.

PR 17-JAN-2001; 2001US-0367358P.

PR 17-JUN-2002; 2002US-0005330.

PR 03-JUN-2002; 2002US-0385691P.

PA (GENE-) GENE-CRAFT INC.

PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

DR WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

XX subject having or suspected of having a malignant condition or a B-cell

XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

CC The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.htm?DocID=20030118592. The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.

XX Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 7; Length 189;

Best Local Similarity 57.2%; Pred. No. 7.7e-53;

Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLEPEAPQVQDESRRWLKAVLRPHLSRFAMVALGLTVILMSLWYQRL 60  
DB 1 MTDSTVITSMLEPRTAQNDYGPQKSSSRPSCSLVALNALGLTAVLVSLLYQWIL 60  
QY 61 CGGSDSTCSHCPCPIILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLTFPDNGVK 120  
DB 61 CGGSYSTCASCPCPDWMKYGNNHCYFYSVEKDWNSSLKFCARDSLHLVITDNGWS 120  
QY 121 LFGELYGDFFWIGLRNIDGRWEGPALS-LRILNLSLQRCGAIHRNGLOASSCEVAL 179  
DB 121 LQVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPL 180  
QY 180 QWICKKV 186  
DB 181 HWCKKV 187

RESULT 6  
ID ADY19892 standard; protein; 189 AA.

XX ADY19892;  
XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 5698.

DE Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
XX Antirheumatic; Antidiabetic; Osteopathic; Hemostatic; Antineoplastic;  
XX Antithrombotic; Antidiabetic; Nephrotoxic; CNS-Gen.; Hepatotoxic;  
XX Vincristine; Gastrointestinal-Gen.; Antipneumatic; Antineoplastic;  
XX Antiallergic; diagnosis.

OS Homo sapiens.

PN WO2005016962-A2.

PD 24-FEB-2005.

PF 11-AUG-2004; 2004WO-US026249.

PR 11-AUG-2003; 2003US-0493546P.

PA (GENTH ) GENENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

DR WPI; 2005-182330/19.

PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 5698; 158pp; English.

CC The invention relates to an isolated nucleic acid encoding a PRO  
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
CC composition, and method are useful for diagnosing and treating an immune  
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 9; Length 189;

Best Local Similarity 57.2%; Pred. No. 7.7e-53;

Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLEPEAPQVQDESRRWLKAVLRPHLSRFAMVALGLTVILMSLWYQRL 60  
DB 1 MTDSTVITSMLEPRTAQNDYGPQKSSSRPSCSLVALNALGLTAVLVSLLYQWIL 60  
QY 61 CGGSDSTCSHCPCPIILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLTFPDNGVK 120  
DB 61 CGGSYSTCASCPCPDWMKYGNNHCYFYSVEKDWNSSLKFCARDSLHLVITDNGWS 120  
QY 121 LFGELYGDFFWIGLRNIDGRWEGPALS-LRILNLSLQRCGAIHRNGLOASSCEVAL 179  
DB 121 LQVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPL 180  
QY 180 QWICKKV 186  
DB 181 HWCKKV 187

RESULT 7  
ID AAM88265 standard; protein; 189 AA.

XX AAM88265;

XX 29-MAR-1999 (first entry)

DE Human mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA, splice variant; human;  
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.



OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Pepcide 7..10  
 FT /note="ITIM motif"  
 FT Modified-site 65..67  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site 97..99  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site 137..139  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site 150..152  
 FT /note="Asn is N-glycosylated"  
 FT  
 PN MO9654209-A2.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 29-MAY-1998; 98WO-GB001572.  
 XX  
 PR 31-MAY-1997; 97GB-00011148.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Hewlett EL, Lamers MBAC, Lamont A, Williams DH;  
 XX  
 DR WPI; 1999-059806/05.  
 XX  
 DR N-PSDB; AAV84198.  
 XX  
 XX  
 PT New polypeptide having a sequence corresponding to human mast cell  
 PT function-associated antigen - useful in forming and manufacturing  
 PT pharmaceutical compositions in the treatment of inflammatory and allergic  
 PT diseases, and tumour growth.  
 XX  
 PS Disclosure; Fig 1; 44pp; English.  
 XX  
 PS This is the amino acid sequence of human mast cell function- associated  
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)  
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line  
 CC KU812 or cDNA derived from human lung tissue. The encoded protein is  
 CC similar to the rat form (see AAW88277) having an intracellular domain  
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and  
 CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see  
 CC AAW88266-67) of human MAFA have been identified. Polypeptides and  
 CC synthetic peptides (see AAW88258-64) based on these truncated MAFA  
 CC proteins can be used in methods for the treatment of inflammatory and  
 CC allergic diseases, and tumour growth  
 CC  
 XX  
 SQ Sequence 189 AA;

Query Match 53.3%; Score 548.5; DB 2; Length 189;  
 Best Local Similarity 55.6%; Pred. No. 1.1e-50;  
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPQVODSRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMRYRL 60  
 DB 1 MTDSVIYSMELPRTAQNDYGPQOKSSSSKSCCLVAITGLLTAVLSTVLYQWIL 60  
 QY 61 CCGSKDSTGSHCPSCPIILMTWNGSHCYFYSMEKKDWNSSLFKCADKSGSHLTPPDNGVK 120  
 DB 61 CCGSNYSTCASCPSPRMWKKYGNHCYFVSVEKKDWNSSLEFCLADSHLVTITDQEMS 120  
 QY 121 LFGELYGDPTWYIGLNINDGWRWEGGPAISL-RIITNSLIORCGAIHRNGLQASSCEVAL 179  
 DB 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPILNFSRISNSFVQTGALINKGLQASSCEVPL 180  
 QY 180 QWICKKV 186  
 DB 181 HGVCCKV 187

ID AAE11759 standard; protein; 189 AA.  
 XX  
 AC AAE11759;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human mast cell function associated antigen (MAFA) protein.  
 XX  
 KW Human; pharmaceutical composition; mast cell function associated antigen;  
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
 KW immunosuppressive; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200170805-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 16-MAR-2001; 2001WO-US008596.  
 XX  
 PR 17-MAR-2000; 2000US-0190716P.  
 XX  
 PA (GEMI-) GEMINI SCI INC.  
 XX  
 PI Takahashi N, Mikayama T;  
 XX  
 DR WPI; 2001-611482/70.  
 XX  
 DR N-PSDB; AAD18734.  
 XX  
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic  
 PT activity of natural killer cell or T-cell, comprises an agent that binds  
 PT to mast cell function-associated antigen ligand on target cell.  
 XX  
 PS Claim 10; Page 18; 49pp; English.  
 XX  
 PS The present invention relates to a pharmaceutical composition comprising  
 CC an agent which specifically binds to a mast cell function associated  
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA  
 CC ligand and a pharmaceutically acceptable excipient. The invention is  
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA  
 CC binding to a ligand on a target cell, by contacting the pharmaceutical  
 CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is human MAFA protein  
 CC  
 XX  
 SQ Sequence 189 AA;

Query Match 53.3%; Score 548.5; DB 4; Length 189;  
 Best Local Similarity 55.6%; Pred. No. 1.1e-50;  
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPQVODSRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMRYRL 60  
 DB 1 MTDSVIYSMELPRTAQNDYGPQOKSSSSKSCCLVAITGLLTAVLSTVLYQWIL 60  
 QY 61 CCGSKDSTGSHCPSCPIILMTWNGSHCYFYSMEKKDWNSSLFKCADKSGSHLTPPDNGVK 120  
 DB 61 CCGSNYSTCASCPSPRMWKKYGNHCYFVSVEKKDWNSSLEFCLADSHLVTITDQEMS 120  
 QY 121 LFGELYGDPTWYIGLNINDGWRWEGGPAISL-RIITNSLIORCGAIHRNGLQASSCEVAL 179  
 DB 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPILNFSRISNSFVQTGALINKGLQASSCEVPL 180  
 QY 180 QWICKKV 186  
 DB 181 HGVCCKV 187





DB 176 LMTREPVCSK MAY 188

RESULT 11

ABBI7910

XX ABBI7910 standard; protein; 189 AA.

AC

XX ABBI7910;

DT 23-JAN-2002 (first entry)

XX

DE Human nervous system related polypeptide SEQ ID NO 6567.

XX

KW Human; nocrotropic; neuroprotective; cytosolatic; dermatological; viroicide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antistickling; antianaemic; antidiabetic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;

KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX

PN WO200159063-A2.

XX

PD 16-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001334.

XX

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 26-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225577P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0231415P.

PR 08-SEP-2000; 2000US-0231416P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0233399P.

PR 14-SEP-2000; 2000US-0233400P.

PR 14-SEP-2000; 2000US-0233401P.

PR 14-SEP-2000; 2000US-0233633P.

PR 14-SEP-2000; 2000US-0233644P.

PR 14-SEP-2000; 2000US-0233655P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235835P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237033P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 20-OCT-2000; 2000US-0242221P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0244647P.

PR 08-NOV-2000; 2000US-02446475P.

PR 08-NOV-2000; 2000US-02446476P.

PR 08-NOV-2000; 2000US-02446478P.

PR 08-NOV-2000; 2000US-02446479P.

PR 08-NOV-2000; 2000US-02446523P.

PR 08-NOV-2000; 2000US-02446524P.

PR 08-NOV-2000; 2000US-02446525P.

PR 08-NOV-2000; 2000US-02446526P.

PR 08-NOV-2000; 2000US-02446528P.

PR 08-NOV-2000; 2000US-02446532P.

PR 08-NOV-2000; 2000US-02446609P.

PR 08-NOV-2000; 2000US-02446610P.

PR 08-NOV-2000; 2000US-02446611P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.







DT 06-NOV-2001 (first entry)  
XX  
DE Human protein SEQ ID NO 1337.  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200157190-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-US004098.  
XX  
PR 03-FEB-2000; 2000US-00496914.  
XX  
PR 27-APR-2000; 2000US-00560875.  
XX  
PR 20-JUN-2000; 2000US-00598075.  
XX  
PR 19-JUL-2000; 2000US-00620325.  
XX  
PR 01-SEP-2000; 2000US-00654936.  
XX  
PR 15-SEP-2000; 2000US-00663561.  
XX  
PR 20-OCT-2000; 2000US-00693325.  
XX  
PR 30-NOV-2000; 2000US-00728422.  
XX  
PA (HUSE-) HUSEQ INC.  
XX  
PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,  
PI Ma Y, Zhao Q, Wang D, Zhang J, Ren F, Chen R, Wang ZW,  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
DR MPI: 2001-476283/51.  
XX  
DR N-PSDB; AAK51808.  
XX  
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
XX  
PS Claim 20; Page 3580; 6221pp; English.  
XX  
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAH80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activity/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAH80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX  
SQ Sequence 188 AA;  
XX  
Query Match 13.9%; Score 143.5; DB 4; Length 188;  
XX  
Best Local Similarity 24.5%; Pred. No. 7.6e-07;  
XX  
Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;  
XX  
QY 40 MVALGILTVYL-----MSLWYORIL-----CCGSKD-----ST 68  
DB 5 MIIISGIVLVKAVGMLFLFLFPQIFNKSNDGFTTTRSYGVSQLFGSSSPNGFITT 64  
QY 69 CSHCPSCPIWTRNGSHCYFMEKKDNWSSLKFCADKGSLLTPPDNGVTLFEEYIQ 128  
DB 65 RSYGVCPKDMFEFYQARCFPLSTSESSWESRDFCKGKSTLAIVTPEKLFQDITDA 124  
QY 129 DFWYVGL---RNIDGRWEGGALSLRILITNSLIQRCSAIIHNGU-----QASSCEVALDW 181  
DB 125 EKYFTIGLYHREKGRWMINNSVFNNGVNTNQNQNFCAIT---GLTKTFDAASCDISYKR 181  
QY 182 ICKK 185

DB 182 ICKK 185  
||:|  
RESULT 15  
AAU00671  
ID AAU00671 standard; protein, 188 AA.  
XX  
XX AAU00671;  
AC  
XX 07-SEP-2001 (first entry)  
XX  
DE Human INTERCEPT 289 form 1a polypeptide.  
XX  
XX Human, INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;  
KW skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;  
KW bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;  
KW anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;  
KW malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;  
KW attention deficit disorder; Crohn's disease; gastroenteritis; goitre;  
KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;  
KW muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Domain 7..27  
FT /note="Transmembrane domain"  
FT Domain 28..188  
FT /note="Extracellular domain"  
XX  
PN WO200129088-A1.  
XX  
PD 26-APR-2001.  
XX  
PF 23-JUN-2000; 2000WO-US017386.  
XX  
PR 19-OCT-1999; 99US-00420707.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Mackay CR, Myers PS, Kiret SJ, Fraser CC, Leiby KR;  
XX  
DR MPI: 2001-308477/32.  
XX  
DR N-PSDB; AAS00661.  
XX  
FT New isolated nucleic acid molecule for diagnosis, prevention, and therapy  
FT of human and other animal disorder, or as modulating agent for regulating  
PT cellular processes.  
XX  
PS Claim 8; Fig 2A-2B; 263pp; English.  
XX  
XX The sequence represents human INTERCEPT 289 form 1a polypeptide. This  
CC protein and similar others exhibit the ability to affect growth,  
CC proliferation, survival, differentiation, activity, morphology, or  
CC movement/migration of, e.g. T cells and cells of the heart, liver,  
CC pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph  
CC node, peripheral blood leukocyte, bone marrow or thymus tissue. They can  
CC be used as modulating agents for regulating cellular processes, thus, the  
CC proteins and their associated nucleic acids can be used to prognosticate,  
CC prevent, diagnose, or treat disorders associated with physiological  
CC processes. These disorders include abnormal blood coagulation, asthma,  
CC anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery  
CC disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,  
CC meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,  
CC goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary  
CC embolism and muscular dystrophy. Antibodies to disorders such as these  
CC can be made by providing a polypeptide of the invention to an immuno-  
CC competent vertebrate and harvesting blood or serum from the vertebrate  
XX  
SQ Sequence 188 AA;  
XX  
Query Match 13.9%; Score 143.5; DB 4; Length 188;





His hope and joy

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3009 Seconds  
(without alignments)  
988.409 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPAPQVOD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	81.4	188	2 I59421	mast cell function
2	56	5.4	189	2 S23149	hypothetical prote
3	54.5	5.3	189	2 A95110	acetyltransferase,
4	53.5	5.2	189	2 E64527	hypothetical prote
5	53	5.2	188	1 DUBPC2	dCMP deaminase (EC
6	53	5.2	188	2 G87336	conserved hypochet
7	52.5	5.1	189	2 T19559	hypothetical prote
8	51.5	5.0	188	2 T37454	probable 21.7k pro
9	51.5	5.0	189	2 G97978	conserved hypochet
10	51	5.0	189	2 T02821	probable membrane
11	48.5	4.7	188	2 C86508	hypothetical prote
12	48.5	4.7	188	2 H72114	transcription regu
13	47.5	4.6	188	1 JC2393	phospholipase A2 1
14	47.5	4.6	188	2 T33623	hypothetical prote
15	46.5	4.5	188	2 A72745	hypothetical prote
16	46.5	4.5	189	2 S30039	hypothetical prote
17	46	4.5	189	2 E96569	probable IAA6 prot
18	46	4.5	189	2 S58493	auxin-induced prot
19	46	4.5	189	2 S60587	non-structural pro
20	45.5	4.4	188	2 T17574	hypothetical prote
21	45.5	4.4	189	2 AG1947	hypothetical prote
22	45	4.4	188	2 T33077	hypothetical prote
23	45	4.4	189	2 B64209	peptidyl-kinase hydr
24	45	4.4	189	2 PC1173	histo-blood group
25	45	4.4	189	2 PC1172	histo-blood group
26	44.5	4.3	188	2 D70820	teratocarcinoma-de
27	44.5	4.3	188	2 A39787	dnaf protein homol
28	44.5	4.3	189	2 S34632	hypothetical prote
29	44	4.3	188	2 S74560	hypothetical prote

30	44	4.3	188	2 F82587	dioxynase Xf2210
31	43.5	4.2	189	2 T00401	hypothetical prote
32	43	4.2	189	2 D84342	peptidyl-prolyl is
33	42.5	4.1	188	2 E97104	phospholipase D fa
34	42.5	4.1	188	2 AHI883	hypothetical prote
35	42.5	4.1	188	2 E88951	protein C38C3.8 (1
36	42.5	4.1	188	2 G75326	probable 16S rRNA
37	42.5	4.1	189	2 T25481	hypothetical prote
38	42.5	4.1	189	2 H86083	hypothetical prote
39	42	4.1	188	2 JC6547	high sulfur prote
40	42	4.1	188	2 T37501	hypothetical prote
41	42	4.1	189	2 G72294	conserved hypochet
42	42	4.1	189	2 B29795	circumsporozoite p
43	42	4.1	189	2 G64909	DNA packaging prot
44	42	4.1	189	2 B71542	hypothetical prote
45	42	4.1	189	2 D86909	conserved hypochet

## ALIGNMENTS

```

RESULT 1
I59421
mast cell function associated antigen - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59421
R/Gutmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A/Title: A secretory inhibitory signal transduction molecule on mast cells is another C
A/Reference number: I59421; PMID:96016176; PMID:7568140
A/Accession: I59421
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-188 <RES>
A/Cross-references: UNIPROT:Q64335; UNIPARC:UPI000030101; EMBL:X79812; NID:G1020141; P
C/Genetics:
A/Gene: mafa

Query Match      81.4%; Score 838; DB 2; Length 188;
Best local Similarity 80.7%; Pred. No. 9.2e-75;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY      1 MADSSYSTLELPAPQVODDSRWKLYLHRLPHLSRFAMVALGLTTLTMSLTMTORTL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MADSSYSTLELPAPRVDDDSRWKLYLHRCVSYLVWVALGLTTLTMSLTLYQRTL 60

QY      61 CGGKXSTGSHCPILMTBNGSHCYFSMEKKDNSSILKFCADKSHLLTPPDNQYK 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 CGGKGFMCSCQCRCPNLWRNGSHCYFSMEKXDNSSILKFCADKSHLLTPPDNQYV 120

QY      121 LFGELYGDFFWYGLNINDGMRWEGPALSLRLITNSLIRQCGAHRNGLOASSCEVALQ 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 LFGELYGDFFWYGLADIDGMRWEDPALSLTSLNSVYQKGTIRCGHASSCEVALQ 180

QY      181 WICKKVL 187
      |||:|||||
Db      181 WICKKVL 187

RESULT 2
S23149
hypothetical protein 3 (nuc 3' region) - Shigella flexneri plasmid psa
C/Species: Shigella flexneri
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C/Accession: S23149
R/Cloze, S.M.; Kado, C.I.
submitted to the EMBL Data Library, March 1992
A/Description: A gene near the plasmid psa origin of replication encodes a nuclease.
A/Reference number: S23149
A/Accession: S23149
A/Molecule type: DNA
A/Residues: 1-189 <CLO>

```

A:Cross-references: UNIPROT:P29772; UNIPARC:UPI00000000DA3; GB:U30471; EMBL:M81325; NID:G  
C:Genetics:  
A:Genome: plasmid  
C:Superfamily: Shigella flexneri plasmid psa hypothetical protein 3 (nuc 3' region)

Query Match  
Best Local Similarity 27.5%; Score 56; DB 2; Length 189;  
Matches 19; Conservative 9; Mismatches 35; Indels 6; Gaps 2;

QY 10 LELPF-APQVQDESFWKKAVALHRPHLSRFAMVALGLTVILMSLIMTORILCCSGKOST 68  
DB 30 LELPQIVPAMNBEVVRPLFVPMHPDAFMTASNAOSDFIVYVNGLAIFYRAMVALGVEDS- 88

QY 69 CSHCPSCPT 77  
DB 89 ----QACPL 93

RESULT 3  
A95110  
acetyltransferase, GNA1 family [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 31-Dec-2004  
C:Accession: A95110  
R:Tellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Author: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: A95110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-189 <KUR>  
A:Cross-references: UNIPROT:Q97R76; UNIPARC:UPI00000051661; GB:AE005672; PIDD:AAK75074.1;  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0953  
C:Superfamily: ribosomal protein serine N-acetyltransferase

Query Match  
Best Local Similarity 26.4%; Score 54.5; DB 2; Length 189;  
Matches 24; Conservative 16; Mismatches 38; Indels 13; Gaps 5;

QY 95 DNSSSLKFCADKSGSHLLTFPDNGVK--LFGEYIGQDFYWGILNIDGMRGSPALSLRIL 154  
DB 28 DAEAMFDVASDKGNTRYPTPTQSLKETNNIAQ--FY--LANPLG-RW-----GIEIK 76

QY 155 TNSLIORCGAIHRNGAQSSCEVALQWICK 185  
DB 77 SNG--QFISTIDLHKIDSVLKRAAIGYIINK 105

RESULT 4  
E64527  
hypothetical protein HP0061 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: E64527  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna  
Nature 388, 539-547, 1997  
A:Author: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: E64527  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-189 <TOM>  
A:Cross-references: UNIPROT:O24901; UNIPARC:UPI000000C07D9; GB:AE000528; GB:AE000511; NID

Query Match  
Best Local Similarity 31.9%; Score 53.5; DB 2; Length 189;  
Matches 23; Conservative 9; Mismatches 25; Indels 15; Gaps 4;

QY 94 KDNSSSLKFCADKSGSHLLTFPDNGVK--LFGEYIGQDFYWGILNIT-----DGWRW 143  
DB 99 KDNWLSLTKI-BDKRSNSL-----GNGTKKLLTNADIGSDYKTVIDSMKTYHQSQOEKTKR 153

QY 144 ECGPALSLRIIT 155  
DB 154 ERGETLEVRPTT 165

RESULT 5  
DUBPC2  
dCMP deaminase (EC 3.5.4.12) - phage T2  
N:Alternate names: deoxycytidylate deaminase  
C:Species: phage T2  
A:Note: host Escherichia coli  
C:Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 09-Jul-2004  
C:Accession: A01011  
R:Maley, G.F.; Guarino, D.U.; Maley, F.  
J. Biol. Chem. 258, 8290-8297, 1983  
A:Title: Complete amino acid sequence of an allosteric enzyme, T2 bacteriophage deoxycyt  
A:Reference number: A01011; MUID:83238442; PMID:6345541  
A:Accession: A01011  
A:Molecule type: protein  
A:Residues: 1-188 <MAL>  
A:Cross-references: UNIPROT:P0814; UNIPARC:UPI000012902B  
C:Comment: The active enzyme is a hexamer of identical chains.  
C:Comment: This is an allosteric enzyme whose activity is greatly influenced by the end  
C:Superfamily: phage T4 dCMP deaminase  
C:Keywords: allosteric regulation; hexamer; hydrolase

Query Match  
Best Local Similarity 19.8%; Score 53; DB 1; Length 188;  
Matches 16; Conservative 10; Mismatches 23; Indels 32; Gaps 3;

QY 68 TCSHPCSPILMTNG-----SHCYFSMEKKDNMSLKFCAKDGSHLLTFPDNGVKLFG 123  
DB 128 TLSPCPDKAKAIASGIKLVYCTYDKKKKQMDILR-----NAGIEVF- 172

QY 124 EYLQDFYWGILNIDGWRWE 144  
DB 173 -----NVPKLWME 180

RESULT 6  
G87336  
conserved hypothetical protein CC0706 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: G87336  
R:Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: G87336  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-188 <STO>  
A:Cross-references: UNIPROT:O9AANA0; UNIPARC:UPI000000C7138; GB:AE005673; NID:g13421929; P  
A:Genetics:  
A:Gene: CC0706

Query Match  
Best Local Similarity 22.7%; Score 53; DB 2; Length 188;  
Matches 27; Conservative 7; Mismatches 35; Indels 50; Gaps 4;

QY 13 PEAPQVQDESFWKKAVALHRPHLSRFAMVALGLTVILMSLIMTORILCCSGKOSTGSHC 72



A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: AB6491; MUID:20330349; PMID:10871362  
A:Accession: C86508  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-188 <STO>  
A:Cross-references: UNIPROT:Q92944; UNIPARC:UPI00000D4127; GB:BA000008; NID:g6978512; PIDN:  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: YggF  
C:Superfamily: hypothetical protein HI0304

Query Match 4.7%; Score 48.5; DB 2; Length 188;  
Best Local Similarity 40.0%; Pred. No.2.4e+03;  
Matches 14; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

OY 83 GSHCYFSMEKCD-WNSSLKFCADKGSHLTPPDN 116  
| : | | : | | | : | | | : | | |  
DB 150 GNKDVFYSPEEDMLATLVKDLGGKYASLTVPDN 184

RESULT 12

H72114  
transcription regulator, probable CP0633 [imported] - Chlamydophila pneumoniae (strains  
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: H72114; E81555  
R:Kauman, S.; Mitchell, W.; Martche, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.,  
Nature Genet. 21, 385-389, 1999  
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: H72114  
A:Molecule type: DNA  
A:Residues: 1-188 <ARN>  
A:Cross-references: UNIPROT:Q92944; UNIPARC:UPI00000D4127; GB:AE001600; GB:AE001363; NID:  
A:Experimental source: strain CHL029  
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: AB1500; MUID:20150255; PMID:10684925  
A:Accession: E81555  
A:Molecule type: DNA  
A:Residues: 1-188 <REA>  
A:Cross-references: UNIPARC:UPI00000D4127; GB:AE002221; GB:AE002161; NID:g7189543; PIDN:  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: yggF, CP0633  
C:Superfamily: hypothetical protein HI0304

Query Match 4.7%; Score 48.5; DB 2; Length 188;  
Best Local Similarity 40.0%; Pred. No.2.4e+03;  
Matches 14; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

OY 83 GSHCYFSMEKCD-WNSSLKFCADKGSHLTPPDN 116  
| : | | : | | | : | | | : | | |  
DB 150 GNKDVFYSPEEDMLATLVKDLGGKYASLTVPDN 184

RESULT 13

UC23393  
phospholipase A2 inhibitor 31k chain - monocled cobra  
C:Species: Najia najia kaouthia, Najia najia siamensis (monocled cobra)  
C>Date: 24-Feb-1995 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: UC23393  
R:Ohkura, N.; Inoue, S.; Ikeda, K.; Hayaashi, K.  
Biochem. Biophys. Res. Commun. 204, 1212-1218, 1994  
A>Title: The two subunits of a phospholipase A2 inhibitor from the plasma of thailand co  
A:Reference number: UC23393; MUID:95071456; PMID:7980598  
A:Accession: UC23393  
A:Molecule type: protein  
A:Residues: 1-188 <OHK>  
A:Cross-references: UNIPROT:O7L2I1; UNIPARC:UPI000017387C

[illegible]

A; Cross-references: UNIPROT:Q9YEU3; UNIPARC:UPI000005DB7A; DDBJ:AP000059; NID:g5103911;

A; Experimental source: strain K1

C;Genetics:

A;Gene: APE0488

C:Superfamily: Aeropyrum pernix hypothetical protein APE04888

Query Match	Score	DB 2;	Length
4.6%	47;	DB 2;	Length 188;

Best Local Similarity 29.3%; Pred. No. 3.3e+03;  
Matches 22; Conservative 8; Mismatches 23; Indels 22; Gaps 5.

Matches	22;	Conservative	8;	Mismatches	23;	Indels	22;	Gaps	5
---------	-----	--------------	----	------------	-----	--------	-----	------	---

Qy 98 SSLKFCADKG-----SHLLTFPD-NQGVKLFGE-----YLGQDFYWIGLRNIDGW 141

Db 12 SSLRVLLDRGFRFTIIGGTVEYALGSRDLGDDVDLFGEEPPPLEEYY--GVAHELGM 69

QY 142 ---RWEGGPALSLR 152

Db 70 SSGQTWLGTPRLIAR 84

Search completed: January 9, 2006, 15:36:34  
Job time : 20.3009 secs

Job time : 20.3009 secs

This copy is  
for the  
Library of Congress



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 96.4956 Seconds  
(without alignments)

1374.564 Million cell updates/sec

Title: US-09-811-367b-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPAPQVQD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: uniprot\_05.80.\*  
2: uniprot\_sprot.\*  
3: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	088713_MOUSE	088713 mus musculu
2	838	81.4	188	064335_RAT	064335 rattus norv
3	568.5	55.2	189	075613_HUMAN	075613 homo sapien
4	548.5	53.3	189	043198_HUMAN	043198 homo sapien
5	162.5	15.8	188	062193_CHICK	062193 gallus gall
6	162.5	15.8	188	062196_CHICK	062196 gallus gall
7	143.5	13.9	188	01C5A_HUMAN	09ny25 homo sapien
8	143.5	13.9	188	052m11_HUMAN	052m11 homo sapien
9	135.5	13.2	189	08C634_MOUSE	08C634 mus musculu
10	109.5	10.6	189	061969_MOUSE	061969 mus musculu
11	96.5	9.4	189	060503_CAEBR	060503 caenorhabdi
12	83	8.1	188	09W012_DROME	09W012 drosophila
13	78.5	7.6	189	018202_CAEEL	018202 caenorhabdi
14	76	7.4	189	096DR9_HUMAN	096dr9 homo sapien
15	72.5	7.0	188	09W3D8_DROME	09w3d8 drosophila
16	69.5	6.8	189	086129_MYTRD	086129 mytilus edu
17	69.5	6.8	189	03LM07_SILPO	03lm07 silicibacte
18	64	6.2	188	08EC21_SHEON	08ec21 shewanella
19	62	6.0	188	06N1X4_RHOPA	06n1x4 rhodospheudo
20	60.5	5.9	188	04V649_DROME	04v649 drosophila
21	57.5	5.6	188	06QJ81_HUMAN	06qj81 homo sapien
22	57.5	5.6	188	04KBR0_PSEPF	04kbr0 pseudomonas
23	57.5	5.6	189	08NFC2_HUMAN	08nfc2 homo sapien
24	56	5.4	189	07K9P1_GAPIC	07k9p1 brisgella fl
25	56	5.4	189	07K9P1_GAPIC	07k9p1 plasmodium
26	55.5	5.4	189	08GEX9_SCHJA	08gex9 schistosoma
27	55.5	5.4	189	04VZZ1_VIRIU	04vzz1 laesa virus
28	54.5	5.3	188	084R12_ARATH	084r12 arabidopsis
29	54.5	5.3	189	097R76_STRPN	097r76 streptococ
30	54	5.2	188	050MR5_ENTHI	050mr5 entamoeba h
31	54	5.2	189	04RR79_TETNG	04rr79 tetradodon n

32	53.5	5.2	188	07K7K8_CAEEL	07k7k8 caenorhabdi
33	53.5	5.2	188	0511R1_ENTHI	0511r1 entamoeba h
34	53.5	5.2	188	04SVB5_TETNG	04svb5 tetradodon n
35	53.5	5.2	189	024901_HELIPY	024901 helicobacte
36	53	5.2	188	1 DCTD_BPT2	P00814 bacterioph
37	53	5.2	188	0507B3_ENTHI	P00814 bacterioph
38	53	5.2	188	06XW15_CASTR	06xw15 lactuca ser
39	53	5.2	188	09AAAO_CAUCR	09aaa0 caulobacter
40	53	5.2	188	05EWR4_GSAUR	05ewr4 acontias me
41	53	5.2	188	05EWR1_GSAUR	05ewr1 acontias me
42	53	5.2	188	08QCB7_9HIV1	08qcb7 human immun
43	53	5.2	189	05QGT0_HUMAN	05qgt0 homo sapien
44	52.5	5.1	188	068P15_CENSCA	068p15 centruroides
45	52.5	5.1	189	09GWT1_MACFA	09gwt1 macaca fasc

## ALIGNMENTS

```

RESULT 1
088713_MOUSE PRELIMINARY; PRT; 188 AA.
ID 088713_MOUSE PRELIMINARY;
AC 088713;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mast cell function-associated antigen 2F1 (Killer cell lectin-like
DE receptor G1) (MAFA).
GN Name=Klrg1; Synonyms=Mafa, mafa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Scurionath;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-
RT associated antigen', is a lectin-like type II transmembrane receptor
RT expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvevTACFBx; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622; DOI=10.1007/s002510000282;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99077501; PubMed=9862665;
RA Blaszer C., Kaufmann M., Pircher H.;
RT "Virus-activated CD8 T cells and lymphokine-activated NK cells express
RT the mast cell function-associated antigen Mafa, an inhibitory C-type
RT lectin.";
RL J. Immunol. 161:6451-6454(1998).
RN [4]
RX EMBL; AF097357; AAD03718.1; -; mRNA.
RX EMBL; AF317727; AAK40082.1; -; Genomic DNA.
DR EMBL; AJ010751; CAA09342.1; -; mRNA.
DR HSSP; Q13241; 1B6E.
DR Ensembl; ENSMUSG00000030114; Mus musculus.
DR MGI; MGI:1355294; Klrg1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005529; F:sugar binding; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.

```

KW Lectin; Receptor.  
FT CHAIN 2 188 mast cell function-associated antigen  
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;  
(MAFA).  
Query Match 100.0%; Score 1029; DB 2; Length 188;  
Best Local Similarity 100.0%; Pred. No. 6,6e-92;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60  
DB 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60  
QY 61 CCGSDSTCSHCPCPIILMTNNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNGVK 120  
DB 61 CCGSDSTCSHCPCPIILMTNNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNGVK 120  
QY 121 LFGEYLGDFFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASSCEVALQ 180  
DB 121 LFGEYLGDFFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASSCEVALQ 180  
QY 181 WICKKVL 188  
DB 181 WICKKVL 188  
181 WICKKVL 188  
RESULT 2  
ID Q64335\_RAT PRELIMINARY; PRT; 188 AA.  
AC Q64335;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
DE MAFa protein (Mast cell function associated antigen).  
GN Name=Klrg1; Synonyms=MAFA, mafa;  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague Dawley; TISSUE=Testis;  
RX MEDLINE=97240766; PubMed=9120279;  
RA Bocsk J. P., Gutthmann M.D., Pecht I.;  
RT "Analysis of the gene encoding the mast cell function-associated  
antigen and its alternatively spliced transcripts.";  
RT J. Immunol. 158:3235-3243(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96016176; PubMed=7568140;  
RT Gutthmann M.D., Tai M., Pecht I.;  
RT "A secretion inhibitory signal transduction molecule on mast cells is  
another C-type lectin.";  
RT Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).  
DR EMBL, X97191; CAA65829.1; -; Genomic\_DNA.  
DR EMBL, X79812; CAA65208.1; -; mRNA.  
DR EMBL, X97192; CAA65829.1; JOINED; Genomic\_DNA.  
DR EMBL, X97193; CAA65829.1; JOINED; Genomic\_DNA.  
DR EMBL, X97194; CAA65829.1; JOINED; Genomic\_DNA.  
DR EMBL, X97195; CAA65829.1; JOINED; Genomic\_DNA.  
DR PIR, I59421; I59421.  
DR HSSP, P26718; 1KCG.  
DR Ensembl, ENSRNOG0000014918; Rattus norvegicus.  
DR RGD, 61978; Klrg1.  
DR GO, GO:0005529; F:sugar binding; IEA.  
DR InterPro, IPR001304; Lectin\_C.  
DR Pfam, PF00059; Lectin\_C\_1.  
DR SMART, SM00034; CLECT\_1.  
DR PROSITE, PS50041; C\_TYPE\_LECTIN\_2; 1.  
SQ SEQUENCE 188 AA; 21356 MW; ZCC6032D4D020B15 CRC64;  
Query Match 81.4%; Score 838; DB 2; Length 188;

Best Local Similarity 80.7%; Pred. No. 2,6e-73;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60  
DB 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60  
QY 61 CCGSDSTCSHCPCPIILMTNNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNGVK 120  
DB 61 CCGSDSTCSHCPCPIILMTNNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNGVK 120  
QY 121 LFGEYLGDFFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASSCEVALQ 180  
DB 121 LFGEYLGDFFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASSCEVALQ 180  
QY 181 WICKKVL 187  
DB 181 WICKKVL 187  
181 WICKKVL 187  
RESULT 3  
ID Q75613\_HUMAN PRELIMINARY; PRT; 189 AA.  
AC Q75613;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
DE ITIM-containing receptor MAFa-L (Mast cell function-associated antigen  
homolog).  
GN Name=MAFA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99057052; PubMed=9842918;  
RX DOI=10.1002/(SICI)1521-4141(199811)28:11<3755::AID-IMMU3755>3.0.CO;2-3;  
RA Butcher S., Arney K.L., Cook G.P.;  
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene  
complex and expressed by basophils and NK cells.";  
RT Eur. J. Immunol. 28:3755-3762(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99077194; PubMed=9862378;  
RA Hanke T., Corral L., Vance R.E., Pauliet D.H.;  
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-  
associated antigen', is a lectin-like type II transmembrane receptor  
expressed by natural killer cells.";  
RT Eur. J. Immunol. 28:4409-4417(1998).  
DR EMBL, AF081675; AAC32200.1; -; mRNA.  
DR EMBL, AF097358; AAD03719.1; -; mRNA.  
DR HSSP, Q13241; 1B6E.  
DR GO, GO:0004872; F:receptor activity; IEA.  
DR GO, GO:0005529; F:sugar binding; IEA.  
DR InterPro, IPR001304; Lectin\_C.  
DR Pfam, PF00059; Lectin\_C\_1.  
DR SMART, SM00034; CLECT\_1.  
DR PROSITE, PS50041; C\_TYPE\_LECTIN\_2; 1.  
KW Receptor.  
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;  
Query Match 55.2%; Score 568.5; DB 2; Length 189;  
Best Local Similarity 57.2%; Pred. No. 4,4e-47;  
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;  
QY 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60  
DB 1 MTDSVITYMLPLPATAQNDYPOQSSSSSSRCVAVLALGLTIVLMSLTYORIL 60  
QY 61 CCGSDSTCSHCPCPIILMTNNGSHCYFYSMEKDWNSSLKFCADKSHLLTFPDNGVK 120

```
Db 61 COGSNSTGASCSPCDRMMKYGNNHCYVSVEEKDNSSLEFCLARDSHLVTITNOEMS 120
Qy 121 LGEVYLGDGFYWGILGNIDGMWEGGPAISL-RILTNLSLIGRCALIHNGLOAASCEVAL 179
Db 121 LLOVFLSEAFQWIGILNNSGMRWEDSPINFSRISNSIVQTCGALINKGLOAASCEVPL 180
Qy 180 QWICKKV 186
Db 181 HWCKKV 187

RESULT 4
ID 043198 HUMAN PRELIMINARY; PRT; 189 AA.
AC 043198;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mast cell function-associated antigen.
DE Name=MAFA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain; digested lung;
RX MEDLINE=9843875; PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;
RA Lamer M.B., Lamont A.G., Williams D.H.;
RT "Human MAFA has alternatively spliced variants."
RL Biochim. Biophys. Acta 1399:209-212(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Enzyme digested lung;
RA Lamer M.B.A.C., Lamont A.G., Williams D.H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034952; AAC34731.1; -; mRNA.
DR HSSP; Q13241; 1B6E.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0004872; F: receptor activity; TAS.
DR GO; GO:0005529; F: sugar binding; TAS.
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0006968; P: cellular defense response; TAS.
DR GO; GO:0006954; P: inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21075 MW; 15B042AD40B2B4F6 CRC64;

Query Match 53.3%; Score 548.5; DB 2; Length 189;
Best Local Similarity 55.6%; Pred. No. 3.9e-45;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
```

```
Q6ZYP3_CHICK PRELIMINARY; PRT; 188 AA.
ID Q6ZYP3;
AC Q6ZYP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B-1ec protein.
DE Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RX PubMed=15749883;
RA Rogers S.L., Gobel T.W., Vierthoeck B.C., Milne S., Beck S.,
RA Kaufman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec reveals that the NK Complex and the MHC share a common ancestral region."
RT J. Immunol. 174:3475-3483(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken MHC."
RT Thesis (2002), Department of Pathology and Microbiology, University of Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Kaufman J.F.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ634337; CG25421.1; -; mRNA.
DR HSSP; Q9H8F0; 1K9J.
DR GO; GO:0005529; F: sugar binding; IPA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTI-FREEZEIT.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21053 MW; 6AD5AC3C9BB8F440 CRC64;

Query Match 15.8%; Score 162.5; DB 2; Length 188;
Best Local Similarity 24.5%; Pred. No. 1.4e-07;
Matches 45; Conservative 29; Mismatches 89; Indels 21; Gaps 7;
```

```
Qy 11 ELPEAPOVODSRMKLKAVALHRPHLSRFAMVALGLTVILMSILMYORILCCGSKDSTCS 70
Db 3 EYREYRVLG-TMSKRREGSRGACVTFQJLTMVAAYFVLITLITAVF-----AVQAFQ 54
Qy 71 H---CPSCLPLWTRNGSHCYFSMEKKDNSSLKFCADKSGHLLTPPDNGCVLFGELYG 127
Db 55 HPQPCACQCPDMDIGFRKCYFSEDSNMTSSQNGSALGASIAVPSAEDLFTWRHKG 114
Qy 128 QDFTYIGLRNIDG----WRWEGGPAIS--LRITNSLIGRCALIHNGLOAASCEVALQW 181
Db 115 SSPHWGLSR-EGKEHEWENVRNPSLSHLFQVQDGL---CAYIGDAGLSSHSCTRRW 170
Qy 182 ICKK 185
Db 171 VCTK 174
```

```
RESULT 6
Q6ZYP6_CHICK PRELIMINARY; PRT; 188 AA.
ID Q6ZYP6;
AC Q6ZYP6;
```

DT	05-JUL-2004 (TREMBlrel. 27, Created)
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE	B-lec protein.
GN	Name=B-1ec;
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Bone marrow;
RX	PubMed=15749883;
RA	Rogers S.L., Gobel T.W., Viertelboeck B.C., Milne S., Beck S.,
RA	Kaufman J.F.;
RT	"Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT	reveals that the NK Complex and the MHC share a common ancestral
RT	region.";
RL	J. Immunol. 174:3475-3483(2005).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Bone marrow;
RA	Rogers S.L.;
RT	"Characterisation of C-type lectin-like receptors in the chicken
RL	MHC.";
RL	Thesis (2002), Department of Pathology and Microbiology, University of
RL	Bristol, Bristol, United Kingdom.
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Bone marrow;
RA	Kaufman J.F.;
RT	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AJ634334; CAG25418.1; -; mRNA.
DR	HSSP; Q9H8P0; 1K9J.
DR	GO; GO:0005529; F: sugar binding; IEA.
DR	InterPro; IPR02353; Antifreezeit.
DR	InterPro; IPR01304; Lectin_C.
DR	Pfam; PF00059; Lectin_C_1.
DR	PRINTS; PR00356; ANTIFREEZEII.
DR	SMART; SMO0034; CLECT; 1.
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR	PROSITE; PS00641; C_TYPE_LECTIN_1; 1.
SO	SEQUENCE 188 AA; 20957 MW; 9FD5BD29B9F9E41 CRC64;

  

Query Match	15.8%; Score 162.5; DB 2; Length 188;
Best Local Similarity	24.5%; Pred. No. 1.4e-07;
Matches	45; Conservative 29; Mismatches 89; Indels 21; Gaps 7
QY	11 ELPEAPQVQDESRLKAVLHRLPHLSRFPAVVALGLTVIIMSILMTORILICGSKDSTCS 70
DB	3 EVREYEPHYLG-TEWSRRREGSPRGACVFTQLTMAVAFVTLITVAVF-----AVQAFOP 54
QY	71 H---CPSPCLILMTRNGSHCYFSEKEDKDNSSLKFCADKSHLLTPPDNGVYLFPEYLG 127
DB	55 HPQCAQCPFMVIGFRGKCYFSDSESWYSSQNNCSALDASLAVFDSADLSFTNRHKG 114
QY	128 QDFYVIGLRNIDG---WRWEGCPALS--LRITNSLIFORCGAIIHRNGIQASSCEVALQW 181
DB	115 SSPHNVIGLSR-EGKEHMAEWNRRLPLSHLPVQGDGL---CAYLDGAGLSSSHCSARRW 170
QY	182 ICKK 185
DB	171 VCTK 174

  

RESULT 7			
CLC5A_HUMAN	STANDARD;	PRT;	188 AA.
ID	CLC5A_HUMAN		
AC	Q9NYZ5; OSUKO;		
DT	10-MAY-2005 (Rel. 47, Created)		
DT	10-MAY-2005 (Rel. 47, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		

DE C-type lectin domain family 5 member A (C-type lectin superfamily  
DE member 5) (Myeloid DAP12-associated lectin) (MDL-1).  
GN Name=CLEC5A; Synonyms=CLEC5F5, MDL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
CC [1]  
CC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,  
CC INTERACTION WITH TYROBP, AND MUTAGENESIS OF LYS-16.  
CC MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;  
CC RA Bakker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.,  
CC RT "Myeloid DAP12-associated lectin (MDL-1) is a cell surface receptor  
CC involved in the activation of myeloid cells."  
CC Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).  
CC [2]  
CC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
CC Mueller A., Merz H., Feller A.C.;  
CC RT "Expression of MDL-1 in human blood and cell lines."  
CC Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
CC [3]  
CC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
CC RP MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01762;  
CC RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
CC Wagner McPherson C., Layman D., Maas J., Jaeger S., Walker R.,  
CC RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,  
CC RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,  
CC RA Vabnick P., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
CC RA Ozersky P., Bielicki L., Scott K., Holmes A., Harting R., Harris A.,  
CC Strong C.N., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
CC RA Kozlowicz-Reilly A., Leonard A., Minx P., Maupin J., Stromwater C.,  
CC RA Tin-Wollman A.-M., Abbott A., Minx P., Maupin J., Stromwater C.,  
CC RA Lacroix P., Miller N., Johnson D., Murray J., Weisner J.P.,  
CC RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speth J.,  
CC RA Bieri T.A., Nelson J.O., Berkowitz N., Wohldmann P.E., Cook L.L.,  
CC RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Wardis E.R.,  
CC RA Clifton S.W., Chaisoe S.L., Marra M.A., Raymond C., Haugen B.,  
CC RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,  
CC RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.S., Frey T.S.,  
CC RA Baerbach R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,  
CC RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,  
CC RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
CC RA Waterston R.H., Wilson R.K.;  
CC RT "The DNA sequence of human chromosome 7.";  
CC Nature 424:157-164(2003).  
CC [1-] FUNCTION: May be involved in proinflammatory activation of myeloid  
CC cells via TYROBP-mediated signaling in a calcium-dependent manner.  
CC [1-] SUBUNIT: Interacts with TYROBP.  
CC [1-] SUBCELLULAR LOCATION: Type II membrane protein (Probable).  
CC [1-] ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC Name=2;  
CC IsoId=Q9N925-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9N925-2; Sequence=VSP\_012839;  
CC [1-] TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in  
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in  
CC cell lines of other origins. Expression is down-regulated when  
CC monocytes differentiate into dendritic cells.  
CC [1-] SIMILARITY: Contains 1 C-type lectin domain.  
CC [1-]  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: AF139768; AA02491.1; -; mRNA.  
CC DR EMBL: AJ271684; CAB7134.1; -; mRNA.  
CC DR EMBL: AC073647; AA07444.1; -; Genomic DNA.  
CC HSSP: P22897.1; EGG.

DR Ensembl: ENSG00000090269; Homo sapiens.  
 DR HGNC: HGNC:2054; CLEC5A.  
 DR MIM: 604987; -.  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0005488; F: binding; TAS.  
 DR GO: GO:0005686; P: cellular defense response; TAS.  
 DR GO: GO:0007165; P: signal transduction; TAS.  
 DR InterPro: IPR002353; AntifreezeZell.  
 DR InterPro: IPR001304; Lectin\_C.  
 DR Pfam: PF00059; Lectin\_C\_1.  
 DR PRINTS: PR00356; ANTI-FREEZE1.  
 DR SMART: SM00034; CLECT\_1.  
 DR PROSITE: PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS0041; C-TYPE LECTIN\_2; 1.  
 DR KEGG: K04401; Glycoprotein; Immune response; Lectin;  
 KW Signal-anchor; Transmembrane.  
 FT TOPO\_DOM 1 4 Cytoplasmic (Potential).  
 FT TRANSMEM 5 27 protein-anchor for type II membrane  
 FT TOPO\_DOM 28 188 Extracellular (Potential).  
 FT DOMAIN 78 184 C-type lectin.  
 FT CARBOHYD 32 32 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 93 93 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 144 144 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 151 151 N-linked (GLCNAC. .) (Potential).  
 FT DISULFID 71 82 By similarity.  
 FT DISULFID 99 183 By similarity.  
 FT DISULFID 161 175 Missing (in isoform 2).  
 FT VARSPIC 116 116 /FTid=VSP\_012839.  
 FT MUTAGEN 16 16 K->I: Abolishes interaction with TYROBP.  
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
 Query Match 13.9%; Score 143.5; DB 1; Length 188;  
 Best Local Similarity 24.5%; Pred. No. 1e-05;  
 Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;  
 QY 40 MVALGLTLVTL-----MSLMTYQRII-----CCGSKD-----ST 68  
 DB 5 MIISGLIVLVKLVGWTFLFLYFPQIFNKNDGFTTTSYGVTSQIFGSSSPNGFIT 64  
 QY 69 CSHCPSCPIILWTRNGSHCYFFSMKKDWNSLKFCAKXSHLITFPDNGVXLFGEYLQ 128  
 DB 65 RSYGVCPKDMERYQARCFPLSTSSSWNSRDFCKKSGTLAIIVTPKLFLODITDA 124  
 QY 129 DFYWIGL---RNIDGWRMEGPPALSLRLITNSLIQRCGAIHRNGL---QASSCEVALQW 181  
 DB 125 EKYFTGLIYHREKRWKRWNNNSVFNNGVNTNQNFCATL---GLTKTFDAASCDISYR 181  
 QY 182 ICKK 185  
 DB 182 ICEK 185  
 RESULT 8  
 052M11\_HUMAN PRELIMINARY; PRT; 188 AA.  
 ID 052M11\_HUMAN PRELIMINARY; PRT; 188 AA.  
 AC 052M11; HUMAN  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE C-type lectin, superfamily member 5.  
 DE Name: CLEC5A; (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RX NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Testis;  
 RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.,  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywicki M.T., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung and heart;  
 RG NIH MGC Project;  
 RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC093714; AAH93714.1; -, mRNA.  
 KW Lectin.  
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
 Query Match 13.9%; Score 143.5; DB 2; Length 188;  
 Best Local Similarity 24.5%; Pred. No. 1e-05;  
 Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;  
 QY 40 MVALGLTLVTL-----MSLMTYQRII-----CCGSKD-----ST 68  
 DB 5 MIISGLIVLVKLVGWTFLFLYFPQIFNKNDGFTTTSYGVTSQIFGSSSPNGFIT 64  
 QY 69 CSHCPSCPIILWTRNGSHCYFFSMKKDWNSLKFCAKXSHLITFPDNGVXLFGEYLQ 128  
 DB 65 RSYGVCPKDMERYQARCFPLSTSSSWNSRDFCKKSGTLAIIVTPKLFLODITDA 124  
 QY 129 DFYWIGL---RNIDGWRMEGPPALSLRLITNSLIQRCGAIHRNGL---QASSCEVALQW 181  
 DB 125 EKYFTGLIYHREKRWKRWNNNSVFNNGVNTNQNFCATL---GLTKTFDAASCDISYR 181  
 QY 182 ICKK 185  
 DB 182 ICEK 185  
 RESULT 9  
 08C634\_MOUSE PRELIMINARY; PRT; 189 AA.  
 ID 08C634\_MOUSE PRELIMINARY; PRT; 189 AA.  
 AC 08C634;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
 DE library, clone:4922502D21 product:hypothetical C-type lectin domain  
 DE containing protein, full insert sequence (Similar to C lectin-related  
 DE protein A).  
 GN Name=4922502D21Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RX NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Testis;  
 RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.,  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

[2]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis; DOI=10.1038/35055500;  
 RX MEDLINE=1085660; PubMed=11217851; Yoshino M., Itoh M., Ishii Y.,  
 RA Kawaji J., Shingagawa A., Shibata K., Kondo S., Yamana K.,  
 RA Arikawa T., Hara M., Fukunishi Y., Kono H., Adachi S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
 RA Saito T., Okazaki Y., Gotojori T., Bono H., Kaekawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaent T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilting L.,  
 RA Wyshab-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirral L.M., Kamegami A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brasic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L.,  
 RA Kamegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Majlote D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numa K., Okido T., Pavani W.J., Pereira G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sanderlin A., Schneider C., Sempke C.A., Setou M., Shmada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells S.,  
 RA Wilting L.G., Wyshab-Boris A., Yanojima M., Yang I., Yang L.,  
 RA Yvan Z., Zevolen M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawaji J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Haehelzume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingagawa A.,  
 RA Yamanishi A., Yoshino M., Watanabe R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama Y., Nishi K., Katsunari T., Taahito H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama T., Nishino T., Harada A.,

RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujisake S., Inoue K., Togawa Y., Irawa M., Ohara E., Matsubiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.",  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hiramoto K., Hirooka T., Hirozane W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiramoto T., Katsurawa T.,  
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kikunaga T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Okazaki Y.,  
RA Saeki R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akibira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Yuramatsu M., Hayashizaki Y.,  
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
[7]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RC MEDLINE=22388257; PubMed=14779932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins J.E., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefter C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dichtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stedman M., Soares M.B., Bonaldi M.F., Casavant T.L., Prange C.,  
RA Birstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pearce C.,  
RA Rata S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buttefield A.J., Schein J.N., Krzyzanski M.I., Skelton S., Smallus D.E.,  
RA Schmechel A., Schein J.B., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[8]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RA Director MGC Project;  
RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK076635; BAC36425.1; -, mRNA.  
DR EMBL; BC089479; AA889479.1; -, mRNA.  
DR Ensembl; ENSMUSG00000047720; Mus musculus.  
DR MGI; MGI:2685920; 492250D21Rik.  
DR GO; GO:0005529; F-actin binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00009; Lectin\_C; 1.  
DR SMART; SM00034; CLCCT; 1.  
DR PROSITE; PSS0041; C\_TYPE\_LECTIN\_2; 1.  
RC Hypothetical protein; Lectin.  
RC SEQUENCE 189 AA; 22107 MW; 2EE5673DBAC2B39B CRC64;

Query Match	13.2%	Score 135.5;	DB 2;	Length 189;
Match Similarity	25.3%	Pred. No. 6.1e-05;		
Bases	48;	Conservative	29;	Mismatches 84;
			Indels	29;
			Gaps	10;
Oy	13	PEAFVODSESRMKLAVLHRPHLSRFAMVAL-----GLTIVILMSLMTYOR--ILCGSGK	65	
Db	7	PRLEQTSHERRH-----HRLMPDAKKVLLTLMTLGGVAVLTLGPFSPFKFTVTRTAR	60	
Oy	66	DSTC-SHCPSPIILMTNGSHCYIFSNKEDQWNSLKFCDKSGHLLTFPNQGVK-LFG	123	



RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,  
 RA Foster C., Garfield A.E., Garg N.S., Gelbart W.M., Glaser K.,  
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Houten D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaisl M., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laasop P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Mozhreva A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195 (2000).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
 RT *melanogaster* euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kamlirker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kamlirker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.-J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Berkeley *Drosophila* Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Flybase; (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 RN Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 RC STRAIN=Berkeley;

RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacle J.,  
 RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;  
 RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; AE003471; AAF47464.1; -, Genomic\_DNA.  
 DR EMBL; BT012477; AAS93748.1; -, mRNA.  
 DR HSSP; P08661; 1BV4.  
 DR Ensemble; CG9134; *Drosophila melanogaster*.  
 DR Flybase; FBgn003159; CG9134.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR01304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C\_1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN\_1.  
 DR PROSITE; PS00411; C TYPE LECTIN 2; 1.  
 SQ SEQUENCE 188 AA; 21848 MW; 51B6C20B2C039DE CRC64;

Query Match 8.1%; Score 83; DB 2; Length 188;  
 Best local similarity 19.7%; Pred. No. 7.8;  
 Matches 36; Conservative 31; Mismatches 66; Indels 50; Gaps 10;

QY 49 ILMSLWYQRLICGSK-----DSTCHSCPSC-----PLMT-----RNGSHCYFF 89  
 DB 5 LILSVLSQLCLIDRTMATPPKPGFVADCPNCVDSQYTPNKMTPLLKLGKRYLL 64  
 QY 90 SM-EKKDWNSSLRKCADKSHLTFFPDNQ-----GVKLFGEYLGDFFYWG----- 134  
 DB 65 GIFFKAWNFKATQYCRHYGMHLASISQGEHNDRLKHKIRDG--LGHHPWISGTDLADE 122  
 QY 135 -----LNIDGWRGEGPALSIRITNSLIDRCGAI-HRNG---LQASSCVALQW 181  
 DB 123 GNFFWMTGATRTFTTNMAGSPNNFR-YENGEBEENCLELWNRDGLKWNDSPCSFETFF 181  
 QY 182 ICK 184  
 DB 182 VCE 184

## RESULT 13

018202 CAEEL PRELIMINARY; PRT; 189 AA.

AC 018202;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein Y48B1B.9.  
 GN ORFNames=Y48B1B.9;  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RG The C. elegans sequencing consortium;

RT "Genome sequence of the nematode *C. elegans*: a platform for

RT investigating biology.";

RL Science 282:2012-2018(1998).

DR EMBL; Z93393; CAB07697.2; -, Genomic\_DNA.

DR PIR; T27020; T27020.

DR HSSP; P22030; 1FVU.

DR WormBase; WBGene0013008; Y48B1B.9.

DR WormPeP; Y48B1B.9; CE36239.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR01304; Lectin\_C.

DR Pfam; PF00059; Lectin\_C\_1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00411; C TYPE LECTIN 2; 1.

DR Complete proteome; Hypothetical protein.

DM SEQUENCE 189 AA; 21548 MW; 192DA964586072FO CRC64;

Query Match 7.6%; Score 78.5; DB 2; Length 189;





RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,  
Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,  
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
Stapleton M., Yamada C., Aeshburner M., Gelbart W.M., Rubin G.M.,  
Lewis S.E.,  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley Drosophila Genome Project;  
RA Celisner S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,  
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RG Flybase;  
RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Friese E.,  
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,  
Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
Celisner S.;  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AE003444; AAF46391.1; -; Genomic\_DNA.  
DR EMBL; AY070795; AAL46417.1; -; mRNA.  
DR HSP; P35247; 1B08.  
DR Ensembl; CG12111; Drosophila melanogaster.  
DR Flybase; FBgn030050; CG1211.  
DR GO; GO:0005529; P:sugar binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
SQ SEQUENCE 188 AA; 21771 MW; 869868CAED1B513A CRC64;  
  
Query Match 7.0%; Score 72.5; DB 2; Length 188;  
Best Local Similarity 18.9%; Pred.No. 82;  
Matches 25; Conservative 24; Mismatches 52; Indels 31; Gaps 7;  
  
QY 79 WTRNGSHCYFS-MEKKQWNSLTKFCADKSHLTFPPDNGVYKLFGEYL-----GDPFY 131  
DB 48 FVRIDNYYIYIEPMKVKVMPQAGACRMNNAHLASIEDKPEMALIKTKAKGFKNIDYF 107  
  
QY 132 WI-----GLRINIDGWR-----WEGGPAISLRILTNLSIQRCAIH-----RNGLOA 172  
DB 108 WISGNDLGTGEGAFYWNMSNGRPMTYAAPWNGPKQMPDNYGNN---ENC--VHMFATREMIN 162  
QY 173 SSCEVALQWICK 184  
DB 163 ANCKIQMLYVCE 174

Search completed: January 9, 2006, 15:35:27  
Job time : 97.4956 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:25:12 ; Search time 25.2885 Seconds  
(without alignment)  
614.628 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSRYSTLELPEAPQVOD.....GLQASSCEVALQWICKVLY 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5.COMB.rep.\*
- 2: /cgn2\_6/prodata/1/iaa/6.COMB.rep.\*
- 3: /cgn2\_6/prodata/1/iaa/H.COMB.rep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCUS.COMB.rep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE.COMB.rep.\*
- 6: /cgn2\_6/prodata/1/iaa/bckfile1.rep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	838	81.4	188	US-08-722-126A-5	Sequence 5, Appl1
2	838	81.4	188	PCT-US95-04258-5	Sequence 5, Appl1
3	52	5.1	188	US-09-543-681A-7232	Sequence 7232, Ap
4	51.5	5.0	188	US-09-902-540-12348	Sequence 12348, A
5	51.5	5.0	189	US-08-469-427A-15	Sequence 15, Appl1
6	49.5	4.8	189	US-09-248-796A-19356	Sequence 19356, A
7	48.5	4.7	188	US-09-438-185A-957	Sequence 957, App
8	47	4.6	189	US-09-438-185A-339	Sequence 339, App
9	46.5	4.5	188	US-08-905-267-2	Sequence 2, Appl1
10	46.5	4.5	188	US-09-314-051-2	Sequence 2, Appl1
11	46.5	4.5	188	US-09-617-389B-2	Sequence 2, Appl1
12	44.5	4.3	188	US-07-749-001-5	Sequence 5, Appl1
13	44.5	4.3	188	US-08-154-198-5	Sequence 5, Appl1
14	44.5	4.3	188	US-08-463-335-5	Sequence 5, Appl1
15	44.5	4.3	188	US-08-464-023A-5	Sequence 5, Appl1
16	44	4.3	188	US-09-134-000C-3652	Sequence 3652, Ap
17	43.5	4.2	188	US-09-252-991A-29925	Sequence 29925, A
18	43.5	4.2	188	US-09-438-185A-761	Sequence 761, App
19	43.5	4.2	189	US-09-198-452A-549	Sequence 549, App
20	43	4.2	188	US-09-122-443-14	Sequence 14, Appl1
21	43	4.2	188	US-07-757-022B-32	Sequence 32, Appl1
22	43	4.2	188	US-09-558-089-14	Sequence 14, Appl1
23	43	4.2	188	US-09-558-087-14	Sequence 14, Appl1
24	43	4.2	188	US-09-248-796A-20257	Sequence 20257, A
25	43	4.2	188	US-09-558-474-14	Sequence 14, Appl1
26	42.5	4.1	188	US-09-252-991A-30309	Sequence 30309, A
27	42.5	4.1	188	US-09-605-703B-1580	Sequence 1580, Ap

## ALIGNMENTS

28	42	4.1	188	US-08-858-207A-497	Sequence 497, App
29	42	4.1	189	US-09-902-540-16146	Sequence 16146, A
30	42	4.1	189	US-09-949-016-10489	Sequence 10489, A
31	41.5	4.0	188	US-09-252-991A-28935	Sequence 28935, A
32	41.5	4.0	188	US-09-270-767-38256	Sequence 38256, A
33	41.5	4.0	188	US-09-270-767-53473	Sequence 53473, A
34	41.5	4.0	189	US-09-270-767-45559	Sequence 45559, A
35	41	4.0	188	US-09-500-569-8	Sequence 8, Appl1
36	41	4.0	188	US-09-971-823B-8	Sequence 8, Appl1
37	41	4.0	188	US-09-248-796A-19379	Sequence 19379, A
38	41	4.0	189	5171685-2	Patent No. 5171685
39	41	4.0	189	5518916-2	Patent No. 5518916
40	40.5	3.9	188	US-09-636-215-592	Sequence 592, App
41	40.5	3.9	188	US-09-685-166A-592	Sequence 592, App
42	40.5	3.9	188	US-09-679-426-592	Sequence 592, App
43	40.5	3.9	188	US-09-759-143-592	Sequence 592, App
44	40.5	3.9	188	US-09-651-236-592	Sequence 592, App
45	40.5	3.9	188	US-09-657-279-592	Sequence 592, App

RESULT 1  
US-08-722-126A-5  
Sequence 5, Application US/08722126A  
Patent No. 6034227  
GENERAL INFORMATION:  
APPLICANT: PECHT, Israel  
APPLICANT: GUTTMANN, Marcelo D.  
APPLICANT: TAL, Michael  
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,126A  
FILING DATE: 08-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04258  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 109257  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: PECHT=1A  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-722-126A-5  
Query Match 81.4%; Score 838; DB 2; Length 188;  
Best Local Similarity 80.7%; Pred. No. 4e+86;

QY 1 MADSSITSLTELPPEAPQVODESRMTKAVILHRPHSLPAMVALGLTIVIMSLMTQRI L 60

Db 1 MADNIIITSLTELPAPAPRVQDDSRMTKAVILHRCSVYLWVALGLTIVIMSLTQRI L 60

QY 61 CCGSKDSTSCSHCPDILMTRNGSHCYYSMEKKDNSSILKFCADYGSHTLTPPDQGVK 120

Db 61 CCGSKGCFMCSQCSRCPNLLMRNGSHCYYSMEKKDNSSILKFCADYGSHTLTPPDQGVN 120

```

0y 77 ILWTRNGSHCYFSEMEKDWNSSLKFCADKSHLLTPFDNGCVKLFEGYLGODPFWIGLR 136
    ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 40 LVMGR-----VRDGMNATREVC-----RLI-----EG-----GKFLPO-----LHLV 72
0y 137 NIDGMREGEPAALSLRLITNSLIRCGAIHNGCLQASSCEVALQ 180

```

Db 73 LLDGIAFGFNVVDLPILASRLKPCVAVWRPPDDIAVERALR 116

RESULT 5  
US-08-469-427A-15

Sequence 15, Application US/08469427A  
Patent No. 5607918

GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf

APPLICANT: Olofsson, Birgitta

APPLICANT: Alltalo, Kari

APPLICANT: Pajusola, Katri

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

TITLE OF INVENTION: DNA CODING THEREFOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKewen, Edwards & Lenahan

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,427A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/397,651

FILING DATE: 01-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Evans, Joseph D

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 41979cp2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 189 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469-427A-15

Query Match 5.0%; Score 51.5; DB 1; Length 189;  
Best Local Similarity 28.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 8; Mismatches 22; Indels 11; Gaps 2;

Db 97 ESNITMQRKPKQSGH-----IERMSFLQHRCECRPKDKTKPENHCEPC 144

RESULT 6  
US-09-248-19356  
Sequence 19356, Application US/09248796A  
Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096, 409

;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 28208  
;; SEQ ID NO 19356  
;; LENGTH: 189  
;; TYPE: PRT  
;; ORGANISM: Candida albicans

;; NAME/KEY: UNSURE  
;; LOCATION: (184), (185)  
;; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown

US-09-248-796A-19356

Query Match 4.8%; Score 49.5; DB 2; Length 189;  
Best Local Similarity 27.3%; Pred. No. 2e+03; Indels 31; Gaps 5;  
Matches 24; Conservative 9; Mismatches 24

Db 93 KKDMSLKFCDKSGSHL---LTFPDNGVKLFG--EYGDGFYWLGNIDGWRWEGP 147

Db 102 KLTYSFLQNCRTNHTMAQINFCKNSAVELFGINETLG---YGVGFYV----- 149

Db 148 ALSRLITNSLIQRCGAH-RNGLOASS 174

Db 150 -----RLAHLRNSINATS 164

RESULT 7  
US-09-438-185A-957  
Sequence 957, Application US/09438185A  
Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kaitman, Sue

APPLICANT: Davis, Ronald

TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US

CURRENT APPLICATION NUMBER: US/09/438, 185A

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/108, 279

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: US 60/128, 606

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 1074

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 957

LENGTH: 188

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

FEATURE:

OTHER INFORMATION: CPN0955

US-09-438-185A-957

Query Match 4.7%; Score 48.5; DB 2; Length 188;  
Best Local Similarity 23.5%; Pred. No. 2.6e+03;  
Matches 16; Conservative 11; Mismatches 20; Indels 21; Gaps 3;

Db 78 LMTNRGSHCYFYFSEKEDMSLFCADKSGSHLT-----FPDNGV---KLF 122

Db 15 LGSRRNRKCSFF-----FSSGTALGKGRGHEHLPSIKLHKKHKKVYLYLDHGIPTEKAY 68

Db 123 GEYLGDPF 130

Db 69 QSLPDPDY 76

RESULT 8  
US-09-438-185A-339  
Sequence 339, Application US/09438185A  
Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kalman, Sue  
APPLICANT: Davis, Ronald  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438,185A  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 60/108,279  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128,606  
PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 1074  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 339  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
OTHER INFORMATION: CPN0337  
US-09-438-185A-339

Query Match 4.6%; Score 47; DB 2; Length 189;  
Best Local Similarity 29.4%; Pred. No. 3.9e+03;  
Matches 15; Conservative 10; Mismatches 20; Indels 6; Gaps 2;

QY 21 ESRWLTAKVLRPHSRF-AMVALGLTYILMSILMYQ-----RLICGSK 65  
DB 112 EERRRKLILHRYELRKLGGKIAQKMTLIPGLMFLSRGVYVRIGCCRGK 162

RESULT 9  
US-08-905-267-2  
Sequence 2, Application US/08905267  
Patent No. 5959075  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Weinberg, Anna C.  
APPLICANT: Lofton-Day, Catherine E.  
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,267  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-06  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6678  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-905-267-2

Query Match 4.5%; Score 46.5; DB 1; Length 188;  
Best Local Similarity 30.8%; Pred. No. 4.4e+03;  
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTGCHGSCPIWTRNGSHCYFSMEKKDNNLSLKFCADKSHLLTFPDNGGV 119  
DB 4 LCC-----SC-LLMWL--GILLAPFSQOEVTSPYKLC---GRDLIV---EVI 42

QY 120 KLFGF 124  
DB 43 KLCCG 47

RESULT 10  
US-09-314-051-2  
Sequence 2, Application US/09314051  
Patent No. 6183991  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Weinberg, Anna C.  
APPLICANT: Lofton-Day, Catherine E.  
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/314,051  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-06  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6678  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-314-051-2

Query Match 4.5%; Score 46.5; DB 2; Length 188;  
Best Local Similarity 30.8%; Pred. No. 4.4e+03;  
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTGCHGSCPIWTRNGSHCYFSMEKKDNNLSLKFCADKSHLLTFPDNGGV 119  
DB 4 LCC-----SC-LLMWL--GILLAPFSQOEVTSPYKLC---GRDLIV---EVI 42

QY 120 KLFGF 124  
DB 43 KLCCG 47

RESULT 11  
US-09-617-389B-2

```
/ Sequence 2, Application US/09617389B
/ Patent No. 6709659
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Conklin, Darrell C.
/ APPLICANT: Lofton-Day, Catherine E.
/ TITLE OF INVENTION: Antibodies That Bind Testis-Specific
/ FILE REFERENCE: 96-06C3
/ CURRENT APPLICATION NUMBER: US/09/617,389B
/ CURRENT FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/339,148
/ PRIOR FILING DATE: 1999-06-24
/ PRIOR APPLICATION NUMBER: 08/905,267
/ PRIOR FILING DATE: 1997-01-18
/ PRIOR APPLICATION NUMBER: 60/023,213
/ PRIOR FILING DATE: 1996-02-08
/ PRIOR APPLICATION NUMBER: 60/031,592
/ PRIOR FILING DATE: 1996-11-21
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ US-09-617-389B-2

Query Match
Best Local Similarity 4.5%; Score 46.5; DB 2; Length 188;
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTCSPCPILWTRNGSHCYPSMEKQWNSLKPCKADKSHLTFPPNGV 119
Db 4 LCC-----SC-LFWL--GLLAPRSGQSEVTSPTKLC--GRDLLV----EVI 42

QY 120 KLFGE 124
Db 43 KLCQG 47

RESULT 12
US-07-749-001-5
/ Sequence 5, Application US/07749001
/ Patent No. 5264557
/ GENERAL INFORMATION:
/ APPLICANT: Salomon, David S.
/ APPLICANT: Persico, Maria G.
/ TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN, DABY & CUSHMAN
/ STREET: 1615 L Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/749,001
/ FILING DATE: 19910823
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Scott, Watson T.
/ REGISTRATION NUMBER: 26,581
/ REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 248453 CUSH
```

```
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 188 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-07-749-001-5

Query Match
Best Local Similarity 4.3%; Score 44.5; DB 1; Length 188;
Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDSRWKAKAVLRPHLSRFANWALGLTVILMSLWQRI--LCCGSKDSTC---SHCP 73
Db 47 RDDSIMPQEEPAIRPSSQ-----RVLPMGIQHSKEINRTCC-LNEGTCMLGSCFA 96

QY 74 SCPILWTRNGSH 85
Db 97 CPSPFYGRNCEH 108

RESULT 13
US-08-154-198-5
/ Sequence 5, Application US/08154198
/ Patent No. 5620866
/ GENERAL INFORMATION:
/ APPLICANT: SALOMON, David S.
/ APPLICANT: PERSICO, Maria G.
/ TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: Stewart Street Tower, One Market Plaza
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: US
/ ZIP: 94105-1493
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/154,198
/ FILING DATE: 17-NOV-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,001
/ FILING DATE: 23-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baetian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 15280-63-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 188 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-154-198-5

Query Match
Best Local Similarity 4.3%; Score 44.5; DB 1; Length 188;
Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDSRWKAKAVLRPHLSRFANWALGLTVILMSLWQRI--LCCGSKDSTC---SHCP 73
Db 47 RDDSIMPQEEPAIRPSSQ-----RVLPMGIQHSKEINRTCC-LNEGTCMLGSCFA 96

QY 74 SCPILWTRNGSH 85
Db 97 CPSPFYGRNCEH 108
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using BW model

Run on: January 9, 2006, 15:35:43 ; Search time 72.5361 Seconds  
(without alignments)  
1082.906 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSISTYLELPEAPQVOD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 6603

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA, Main:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	US-09-811-367B-3	Sequence 3, Appli
2	838	81.4	188	US-09-811-367B-5	Sequence 3, Appli
3	568.5	55.2	189	US-10-207-655-196	Sequence 16, App
4	568.5	55.2	189	US-10-756-149-5210	Sequence 5210, Ap
5	548.5	53.3	189	US-09-811-367B-1	Sequence 1, Appli
6	152	14.8	189	US-09-764-870-487	Sequence 487, App
7	152	14.8	189	US-10-125-540-487	Sequence 487, App
8	143.5	13.9	188	US-09-759-130B-83	Sequence 83, Appl
9	143.5	13.9	188	US-10-287-436A-69	Sequence 69, Appl
10	143.5	13.9	188	US-10-287-436A-1251	Sequence 1251, Ap
11	143.5	13.9	188	US-11-097-143-5490	Sequence 5490, Ap
12	83	8.1	188	US-11-097-143-5490	Sequence 3261, Ap
13	72.5	7.0	188	US-10-114-893-48	Sequence 48, Appl
14	69.5	6.8	189	US-10-425-115-345243	Sequence 345243,
15	61.5	6.0	189	US-10-424-599-250285	Sequence 250285,
16	59.5	5.8	188	US-10-767-701-56009	Sequence 56009, A
17	56.5	5.5	188	US-10-437-963-202199	Sequence 202199,
18	56	5.4	189	US-10-424-599-260240	Sequence 260240,
19	55.5	5.4	188	US-10-424-599-260240	Sequence 18766, Ap
20	54.5	5.3	189	US-10-472-928-1876	Sequence 190542,
21	54	5.2	188	US-10-437-963-190542	Sequence 248, App
22	53.5	5.2	189	US-09-895-913A-248	Sequence 37926, A
23	52.5	5.1	189	US-10-450-763-37926	Sequence 4950, Ap
24	52	5.1	188	US-09-738-626-4950	Sequence 3103, Ap
25	52	5.1	189	US-10-108-260A-3303	Sequence 34822, A
26	52	5.1	189	US-10-767-701-34822	Sequence 157696,
27	51.5	5.0	188	US-10-424-599-157696	

28	51.5	5.0	188	US-10-450-763-32442	Sequence 32442, A
29	51.5	5.0	189	US-10-424-599-226112	Sequence 226112,
30	51.5	5.0	189	US-10-767-701-37569	Sequence 37569, A
31	51	5.0	188	US-10-767-701-43351	Sequence 43351, A
32	50	4.9	189	US-10-074-566-66	Sequence 66, Appl
33	50	4.9	189	US-10-074-566-74	Sequence 74, Appl
34	49.5	4.8	188	US-10-389-566-909	Sequence 909, App
35	49	4.8	188	US-09-798-889-110	Sequence 130, App
36	49	4.8	188	US-10-633-680-130	Sequence 130, App
37	49	4.8	188	US-10-424-599-152847	Sequence 152847,
38	49	4.8	188	US-10-424-599-235426	Sequence 235426,
39	49	4.8	188	US-10-424-599-270985	Sequence 270985,
40	49	4.8	189	US-10-425-114-38940	Sequence 38940, A
41	49	4.8	189	US-10-425-115-242970	Sequence 242970,
42	48.5	4.7	188	US-10-425-115-315785	Sequence 315785,
43	48.5	4.7	189	US-10-501-282-1558	Sequence 1558, Ap
44	48	4.7	188	US-10-767-701-50982	Sequence 50982, A
45	48	4.7	188	US-10-425-115-308045	Sequence 308045,

## ALIGNMENTS

```
RESULT 1
US-09-811-367B-3
Sequence 3, Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110A1uaki
APPLICANT: Miyayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
FILE REFERENCE: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
CURRENT APPLICATION NUMBER: US/09/811,367B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 188
TYPE: PRT
ORGANISM: Mus musculus
US-09-811-367B-3

Query Match      100.0%; Score 1029; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 7, 6e-98;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      MADSSISTYLELPEAPQVODSRWKLKAVLHDPHLSRFANVALGLTIVILMSLMTQRI 60
      |||||
DB      1      MADSSISTYLELPEAPQVODSRWKLKAVLHDPHLSRFANVALGLTIVILMSLMTQRI 60

QY      61      CCSKSTKSTCHGCHSCPTLWTRNGSHCYFSEMEKKDNSSLKFCADKSHLLTPDNGVK 120
      |||||
DB      61      CCSKSTKSTCHGCHSCPTLWTRNGSHCYFSEMEKKDNSSLKFCADKSHLLTPDNGVK 120

QY      121     LFGEYLGQDPYVWIGLRIIDGMRWEGGPALEIRLITNSLIRCGAIHNGLOASSCEVALQ 180
      |||||
DB      121     LFGEYLGQDPYVWIGLRIIDGMRWEGGPALEIRLITNSLIRCGAIHNGLOASSCEVALQ 180

QY      181     WICKKVLV 188
      |||||
DB      181     WICKKVLV 188

RESULT 2
US-09-811-367B-5
Sequence 5, Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
APPLICANT: GEMINI SCIENCE, INC.
```

```

; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIORITY FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIORITY FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5
```

```

Query Match      81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 4e-78;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MADNSIYSTLELPAAPRVQDDSRMKVKAVLHRCVSYLMVALGLITVIMSLLYORTL 60

QY      61 CCGSDSTCSHCPCPIILMTNRNGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSGFMCSCQCRPCPNLMNRGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVN 120

QY      121 LFGELYGODFYWIGLRNIDGMRWEGGPAALSLRLITNSLIORCGAIHRNGLOASSCEVALQ 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LFGELYGDEFFYVIGLRNIDGMRWEGGPAALSLRLITNSLVYQKGTIHRGGLHASSCEVALQ 180

QY      181 WICKCKV 187
      |||:|||||
DB      181 WICKCKV 187
```

```

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Havden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; PRIORITY FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196
```

```

Query Match      55.2%; Score 568.5; DB 4; Length 189;
Best Local Similarity 57.2%; Pred. No. 2.7e-50;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MTDSSITSMLELPTATQANDYGPQOKSSSRPSCCLVAIALGLITVALSLVLYQWIL 60

QY      61 CCGSDSTCSHCPCPIILMTNRNGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSNYSTCASCPCPDMMKYGHNHCYFYSVEKMDWNSLKFCLARDSHLLVITDNOGMS 120

QY      121 LFGELYGODFYWIGLRNIDGMRWEGGPAALSLRLITNSLIORCGAIHRNGLOASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LQGVFLSAFCWIGLRNNSGMRWEGGPAALSLRLITNSLIORCGAIHRNGLOASSCEVAL 180
```

```

QY      180 QWICKKV 186
      |||:|||||
DB      181 HMVCKKV 187
```

```

RESULT 4
US-10-756-149-5210
; Sequence 5210, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; PRIORITY FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5210
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5210
```

```

Query Match      55.2%; Score 568.5; DB 5; Length 189;
Best Local Similarity 57.2%; Pred. No. 2.7e-50;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MTDSSITSMLELPTATQANDYGPQOKSSSRPSCCLVAIALGLITVALSLVLYQWIL 60

QY      61 CCGSDSTCSHCPCPIILMTNRNGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSNYSTCASCPCPDMMKYGHNHCYFYSVEKMDWNSLKFCLARDSHLLVITDNOGMS 120

QY      121 LFGELYGODFYWIGLRNIDGMRWEGGPAALSLRLITNSLIORCGAIHRNGLOASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LQGVFLSAFCWIGLRNNSGMRWEGGPAALSLRLITNSLIORCGAIHRNGLOASSCEVAL 180

QY      180 QWICKKV 186
      |||:|||||
DB      181 HMVCKKV 187
```

```

RESULT 5
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIORITY FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIORITY FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1
```

```

Query Match      53.3%; Score 548.5; DB 3; Length 189;
Best Local Similarity 55.6%; Pred. No. 3.1e-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
```

```

Qy      1  MADSSYSTLELPEAPQVODSSRNKTKXVLRPHLSRPAWALGILTVILMSILMYOIL 60
Db      1  MTDVIVYSMTELPTATOQANDYGPOQKSSSSSKPSCCLVAILTGLIVLAVSLVLYOMIL 60
Qy      61  CCSGKSDTSCSHCPSCPIILMTRNGSHCYFFSMEKKDMNSLKFCDKSGHLLTFPDNGCVK 120
Db      61  CGSINYSFCACPCPSCPRMKYKGNHCYFVSBEKDMNSLFCCLARDSHLLVITDNGMS 120
Qy      121  LFGEYLQDFYWIGLRNIDGRWEGGPAISL-RIITNSLIORCGAIHRNGIOASSCEVAL 179
Db      121  LLQVLFSEAFQWIGLRNNSGWRMEDGSPINSRISNSFVQTCGAINRNGIOASSCEVPL 180
Qy      180  QWICKV 186
Db      181  HGVCCKV 187

RESULT 6
US-09-764-870-487
; Sequence 487, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 487
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-487

Query Match      14.8%; Score 152; DB 3; Length 189;
Best Local Similarity 22.3%; Pred. No. 2,7e-07;
Matches 43; Conservative 30; Mismatches 80; Indels 40; Gaps 6

Qy      2  ADSISTYLELPEAP----QVODESRMKLKAVALRPHLSRPAWVALGILTVILMSILMYQ 57
Db      30  SSTAVALALELVDPPGCRNSARDEGSTSKALB----- 63
Qy      58  RILCCGSKDSTCSHCPS-CPIILMTRNGSHCYFFSMEKKDMNSLKFCDKSGHLLTFPDN 116
Db      64  -----ASKG-CIKCEAPCPEDMWLIGKRCYCFPSEBPRMNTGRQYCHTHBAVLAVIQSQ 116
Qy      117  QGVKLFGELYLQDFYWIGLRNIT-DGWRWEGGPAISLRIITNSLIORCGAIHRNGLOASSC 175
Db      117  KLELEFQFKTRRE-PWIGLRVQDBFHWYNGDPFDEFTIAGPGCEVPEPTRLVSTEC 175
Qy      176  EVALQWICKVLY 188
Db      176  LMTRPWVCSKWAY 188

RESULT 7
US-10-125-540-487
; Sequence 487, Application US/10125540
; Patent No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 487
; LENGTH: 189
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-125-540-487

Query Match      14.8% Score 152; DB 4; Length 189;
Best Local Similarity 22.3%; Pred. No. 2.7e-07; Indels 40; Gaps 6;
Matches 43; Conservative 30; Mismatches 80;

OY   2 ADGSIYSTLTLEAP-----QVDESEWKLKAVLHRRPHLSRFAMVALGLTLVIIMSLMYQ 57
     : ::::|::|::|::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB    30 GSTVAALAHLLVPDPCGRNARDEGSTSWMAALE-----                     63

OY   58 RILCCGSKDSTCSHCPS-CPIIWRNGSHCYYSMEKKMNSCLKTCADKGSHLLTFPPDN 116
Db    64 -----ASKG--CIKCACPCEPWLYGRKYCFPSEBRDMNTROYCHTHEAFLAVIQSQ 116
OY   117 QGVVLFEFYIGDPFWYTGIANI-DGMWEQGPLSLRLTNSLIHQCGAIHRGNLOASSC 175
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    117 KEIEFMFKFTFRRE-PWIGLRVGDEFHWANGDDPDPTFIAGBGEVFVEPRIVSTECC 175
OY   176 EVALOWICKKVLY 188
Db    176 LMTRPWCCKMAY 188


RESULT 8
US-09-759-1308-83
Sequence 83, Application US/09759130B
Publication No. US20030022279A1
GENERAL INFORMATION:
APPPLICANT: Millennium Pharmaceuticals, Inc.
APPPLICANT: McCarty, Sean A
APPPLICANT: Fraser, Christopher C
APPPLICANT: Sharp, John D
APPPLICANT: Barnes, Thomas S
APPPLICANT: Kirscht, Susan J
APPPLICANT: Mackay, Charles R
APPPLICANT: Myers, Paul S
APPPLICANT: Leiby, Kevin R
APPPLICANT: Wrighton, Nicolas
APPPLICANT: Goodearl, Andrew
APPPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MP100-53SONAIM
CURRENT APPLICATION NUMBER: US/09/759, 130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
```



```

: CURRENT APPLICATION NUMBER: US/10/287,436A
:
: PRIOR FILING DATE: 2002-10-31
:
: PRIOR APPLICATION NUMBER: US 60/336,220
:
: PRIOR FILING DATE: 2001-10-31
:
: NUMBER OF SEQ ID NOS: 1446
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 1251
:
: LENGTH: 188
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-10-287-436A-1251

```

Query Match	13.9%	Score	143.5	DB	5	Length	188
Similarity	24.5%	Pred	No. 2e-05				
Beet Local	45	Conservative	26	Mismatches	72	Indels	41
Matches						Gaps	6

[illegible]

RESULT 12  
US-11-097-143-5490

; Sequence 5490, Application US/11097143  
 ; Publication No. US20050208558A1  
 ; GENERAL INFORMATION:

1 APPLICANT: Venter, J. Craig  
 2 APPLICANT: et al.  
 3 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
 4 TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
 5 TITLE OF INVENTION: DROSOPHILA GENES.

```

1 CURRENT APPLICATION NUMBER: US/11/097,143
2
3 CURRENT FILING DATE: 2005-04-04
4
5 PRIOR APPLICATION NUMBER: 60/157,832
6
7 PRIOR FILING DATE: 1999-10-05
8
9 PRIOR APPLICATION NUMBER: 60/160,191
10
11 PRIOR FILING DATE: 1999-10-19
12
13 PRIOR APPLICATION NUMBER: 60/161,932
14
15 PRIOR FILING DATE: 1999-10-28
16
17 PRIOR APPLICATION NUMBER: 60/164,769
18
19 PRIOR FILING DATE: 1999-11-12
20
21 PRIOR APPLICATION NUMBER: 60/173,383
22
23 PRIOR FILING DATE: 1999-12-28
24
25 PRIOR APPLICATION NUMBER: 60/175,693
26
27 PRIOR FILING DATE: 2000-01-12
28
29 PRIOR APPLICATION NUMBER: 60/184,831
30
31 PRIOR FILING DATE: 2000-02-24
32
33 PRIOR APPLICATION NUMBER: 60/191,637
34
35 PRIOR FILING DATE: 2000-03-23
36
37 NUMBER OF SEQ ID NOS: 43008
38
39 SOFTWARE: FaSTSeq for Windows Version 4.0
40
41 SEQ ID NO 5490
42
43 LENGTH: 188

```

Query Match 8.1%; Score 83; DB 6; Length 188;  
Best Local Similarity 19.7%; Pred. NO. 3.6;  
Matches 36; Conservative 31; Mismatches 66; Gaps 10;

```

QY 45 ILMSLMQRILCCSGK-----DNRCSHCPSG-----PLMT-----RNSHCYGF 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 LILSVIISIQLLCCLDRYMATPPKPGPGVADCPNCVDSQYTFNKMTPLKLGEKRYL 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 90 SM-EKDMNNSLKFCADKSGSHLLTPPDNQ-----GVKLFGEYLGDFFYIG----- 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 GIFFKANWPRAYQYCKYHGMHLASISQGEENDRLKHIRDFG--LGHNFHISGTDLADE 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 135 -----LRNIDGMWEGPRLSLRILNLSIQRCGL-IRNG-----LQASCEVALQW 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 GNEFFWMAIGRPITFTWNAAGBPNFR-YENGEEBNCLELMNRDQKGLKMDSPCSFETYF 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 ICK 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 VCE 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13  
US-11-097

; Sequence 3261, Application US/11097143  
; Publication No. US20050208558A1

APPLICANT: Venter, J. Craig  
 APPLICANT: et al.  
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
 ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
 TITLE OF INVENTION: DROSOPHILA GENES.

```

1 CURRENT APPLICATION NUMBER: 05/11/097,143
2 CURRENT FILING DATE: 2005-04-04
3 PRIOR APPLICATION NUMBER: 60/157,832
4 PRIOR FILING DATE: 1999-10-05
5 PRIOR APPLICATION NUMBER: 60/160,191
6 PRIOR FILING DATE: 1999-10-19
7 PRIOR APPLICATION NUMBER: 60/161,932
8 PRIOR FILING DATE: 1999-10-28
9 PRIOR APPLICATION NUMBER: 60/164,769
10 PRIOR FILING DATE: 1999-11-12
11 PRIOR APPLICATION NUMBER: 60/173,383
12 PRIOR FILING DATE: 1999-12-28
13 PRIOR APPLICATION NUMBER: 60/175,693
14 PRIOR FILING DATE: 2000-01-12
15 PRIOR APPLICATION NUMBER: 60/184,831
16 PRIOR FILING DATE: 2000-02-24
17 PRIOR APPLICATION NUMBER: 60/191,637
18 PRIOR FILING DATE: 2000-03-23
19 NUMBER OF SEQ ID NOS: 43008
20 SOFTWARE: SeqSeq for Windows Version 4.0
21 SEQ ID NO 3261

```

Query Match	7.0%	Score 72.5	DB 6	Length 188
Best Local Similarity	18.9%	Pred. No. 43		
Matches	25	Conservative	52	Indels 31
		Mismatches		Gaps 7

QY	79 WTRNSHCYYFS-MEKKDNNSLKPCADKGSHLTTPDNQGYVLFGELY-----GDFY 131 : : : :
Db	48 FRIIGNYYYYIPEPNNVYNMFQAAGCRMMNAHLASLEDREEMALIKIMAKGFKNNDYF 107 : : : :
QY	132 WI-----GLRNDGR-----MEGGPALSLRLTNSLORCGAII-----RNGLOA 172          
Db	108 WISGNDLGEGAFYMNMSNGRPMTYAPWNPGRKOMPNYGN---ENC--VHMFATREMIND 162 : : : :
QY	173 SSCCEVALQWICK 184 :: :: :: : :: :: :: :
Db	163 ANCKIQMLTYCE 174 : : : :

## RESULT 14

US-10-114-893-48  
; Sequence 48, Application US/10114893  
; Publication No. US20020193567A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Werberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Bowman, Michael R.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Carlin-Duckett, McKeough  
; APPLICANT: Kelleher, Kerry S.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: GI 6000-10A  
; CURRENT APPLICATION NUMBER: US/10/114,893  
; CURRENT FILING DATE: 2002-04-02  
; EARLIER APPLICATION NUMBER: 09/413,232  
; EARLIER FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-114-893-48

Query Match 6.8%; Score 69.5; DB 4; Length 189;  
Best Local Similarity 23.7%; Pred. No. 89;  
Matches 27; Conservative 20; Mismatches 36; Indels 31; Gaps 5;

QY 3 DSSIVSTLELPE-----APQVDESRLKAVLHRLPRLSRFAMVALGLITVIMSLMYQ 57  
DB 93 EASQSENEILKEMITLARKLNKSKSQWE--LHHQNLN-----LQETL--K 135  
QY 58 RILCGSKDSTCHSPSCPIILWTRNGSHCYFYSMEKXDNSSLKFCADKSHLL 111  
DB 136 RVANCSA-----PCQDWMHGENCYLPSGSPFWNEKSQEKCLSDAXLL 180

RESULT 15  
US-10-425-115-345243  
; Sequence 345243, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 345243  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_78028C.1.pep  
US-10-425-115-345243

Query Match 6.0%; Score 61.5; DB 4; Length 189;  
Best Local Similarity 20.9%; Pred. No. 66+02;  
Matches 24; Conservative 23; Mismatches 41; Indels 27; Gaps 5;

QY 16 PQVDESRLKAVLHRLPRLSRFAMVALGLITVIMSLMYQRIIC-----CGSK 65  
DB 5 PLLLSLGRWISRA--SAPWYLGFCLIALAPRLIVDLVAIFLFQKLCSPMLISNTCGVV 62

QY 66 DSTC-----SHCSPCPIILWTRNGSHCYFYSME-KXDNSSLKFCAD 105  
DB 63 PCLLGEKFLYMAKTAQANCDACQVLDVKEPPSHHSCCEVQANYNERRRGAE 117

Search completed: January 9, 2006, 15:55:59  
Job time : 73.5381 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.6478 Seconds  
(without alignments)  
149.666 Million cell updates/sec

Title: US-09-811-367b-3

Perfect score: 1029  
Sequence: 1 MADSSITSLLEAPQVQD.....GLQASSCEVALQWICKIVLY 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	US-10-055-877-205	Sequence 205, App
2	838	81.4	188	US-10-055-877-206	Sequence 206, App
3	568.5	55.2	189	US-10-055-877-207	Sequence 207, App
4	548.5	53.3	189	US-10-055-877-209	Sequence 209, App
5	56	5.4	189	US-10-416-384-1	Sequence 1, Appl
6	42	4.1	188	US-10-842-206-40	Sequence 40, Appl
7	42	4.1	188	US-10-980-459-32	Sequence 32, Appl
8	41.5	4.0	188	US-10-945-853-2	Sequence 2, Appl
9	40.5	3.9	188	US-10-467-657-2750	Sequence 2750, App
10	40.5	3.9	188	US-10-131-826A-240	Sequence 240, App
11	40.5	3.9	189	US-10-467-657-246	Sequence 246, App
12	40.5	3.9	189	US-10-467-657-2690	Sequence 2690, App
13	37.5	3.6	188	US-10-945-853-1	Sequence 1, Appl
14	37	3.6	188	US-10-821-234-1393	Sequence 1393, Appl
15	37	3.6	188	US-10-528-031-4	Sequence 4, Appl
16	37	3.6	189	US-10-131-826A-232	Sequence 232, App
17	37	3.6	189	US-10-467-657-8250	Sequence 8250, App
18	37	3.6	189	US-11-137-465-60	Sequence 60, Appl
19	36.5	3.5	188	US-11-064-774A-117	Sequence 117, Appl
20	35.5	3.4	189	US-11-100-183-61	Sequence 61, Appl
21	34	3.3	188	US-10-980-388-101	Sequence 101, Appl
22	34	3.3	189	US-10-793-626-2976	Sequence 2976, App
23	34	3.3	189	US-10-793-626-3000	Sequence 3000, App
24	34	3.3	189	US-10-467-657-4044	Sequence 4044, App
25	34	3.3	189	US-11-147-492-14	Sequence 14, Appl

## ALIGNMENTS

25	33.5	3.3	188	US-10-884-730-88	Sequence 88, Appl
27	33.5	3.3	188	US-10-884-730-294	Sequence 294, App
28	33.5	3.3	188	US-10-884-730-332	Sequence 332, App
29	33.5	3.3	188	US-10-793-626-2698	Sequence 2698, App
30	33.5	3.3	189	US-10-995-561-643	Sequence 643, App
31	33.5	3.3	189	US-10-873-528-15	Sequence 15, Appl
32	33	3.2	188	US-11-036-797-37	Sequence 37, Appl
33	33	3.2	189	US-11-147-492-24	Sequence 24, Appl
34	32.5	3.2	188	US-10-821-234-941	Sequence 941, Appl
35	32.5	3.2	189	US-11-205-103-33	Sequence 33, Appl
36	32	3.1	188	US-11-000-463-866	Sequence 866, App
37	32	3.1	188	US-11-000-463-867	Sequence 867, App
38	32	3.1	189	US-10-485-517-221	Sequence 221, App
39	32	3.1	189	US-10-467-657-922	Sequence 922, App
40	32	3.1	189	US-11-147-492-12	Sequence 12, Appl
41	31.5	3.1	189	US-11-147-492-6	Sequence 6, Appl
42	31	3.0	189	US-10-821-234-1421	Sequence 1421, App
43	30.5	3.0	189	US-11-147-492-22	Sequence 22, Appl
44	30	2.9	188	US-10-980-388-90	Sequence 90, Appl
45	30	2.9	188	US-10-467-657-3200	Sequence 3200, App

RESULT 1  
US-10-055-877-205  
; Sequence 205, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:  
; APPLICANT: Decristofaro, Marc  
; APPLICANT: Padigaru, Muraidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zernhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patuvarajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055, 877  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262, 892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263, 598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263, 799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264, 117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264, 139  
; PRIOR FILING DATE: 2001-01-25

```
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 205
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-205
```

```
Query Match      100.0%; Score 1029; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MADSSIVSTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMYQRI 60
DB      1 MADSSIVSTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMYQRI 60
QY      61 CCGSDSTCSHCPCSPILMTNRGSHCYFYSMEKXDMNSLKFCDKSGHLLTFPNOGVK 120
DB      61 CCGSDSTCSHCPCSPILMTNRGSHCYFYSMEKXDMNSLKFCDKSGHLLTFPNOGVK 120
QY      121 LFGELYGDFFYIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
DB      121 LFGELYGDFFYIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
QY      181 WICKKVL 188
DB      181 WICKKVL 188

RESULT 2
US-10-055-877-206
; Sequence 206, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patuturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eiseen, Andrew
; APPLICANT: Molenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
```

```
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-055-877-206
```

```
Query Match      81.4%; Score 838; DB 6; Length 188;
Best Local Similarity 80.7%; Pred. No. 6.7e-84;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```

```
QY      1 MADSSIVSTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMYQRI 60
DB      1 MADSSIVSTLELPEAPQVODESRMKLKAVALHRPCVSYLVAMVALGLITVILMSLMYQRI 60
QY      61 CCGSDSTCSHCPCSPILMTNRGSHCYFYSMEKXDMNSLKFCDKSGHLLTFPNOGVK 120
DB      61 CCGSGFMCQCSRCPCPNMNMNGSHCYFYSMEKXDMNSLKFCDKSGHLLTFPNOGVN 120
QY      121 LFGELYGDFFYIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
DB      121 LFOEYVGBDFYIGLRNIDGWRMEGPGALSLRLTNSLVQKCGTIRCGLHASSCEVALQ 180
QY      181 WICKKVL 187
DB      181 WICKKVL 187

RESULT 3
US-10-055-877-207
; Sequence 207, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
```



```
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patlurajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT FILING DATE: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 207
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-207

Query Match      55.2%; Score 568.5; DB 6; Length 189;
Best Local Similarity 57.2%; Pred. No. 1,le-54;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPVODESRWKLKAVLHRLHLSFAMVAVLGLTVILMSLMTYRIL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDSVIYSMLPLPATQANDYGPQOKSSSRSPSCSLVIAIGLITLAVALLSVLYOWIL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 CCGSKDSTCHSCPCPLIMTRNSHCYFSEMEKKDNNSLKPCADKSHLLTFPDNGVK 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CCGSNVSTCCASCPCPRMKYGNHCYFSEMEKKDNNSLFCCLARDSHLLVITDNGMS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 LFGFYLGGDFYWIGLRINIDGRWEGPALSL-RILTNSLIQRCGAHRRNGLOASSCEVAL 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 LLOVFLSEARFCWIGLRINNSGWRWEDGSPINFSRISNSFYQTGCAIKNGLOASSCEVPL 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 180 QWICKKV 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 HMVCKKV 187
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-10-055-877-209
Sequence 209, Application US/10055877
```

```
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tcherev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Rattelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patlurajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT FILING DATE: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-209

Query Match      53.3%; Score 548.5; DB 6; Length 189;
Best Local Similarity 55.6%; Pred. No. 1,6e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPVODESRWKLKAVLHRLHLSFAMVAVLGLTVILMSLMTYRIL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDSVIYSMLPLPATQANDYGPQOKSSSRSPSCSLVIAIGLITLAVALLSVLYOWIL 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 CCGSKDSTCHSCPCPLIMTRNSHCYFSEMEKKDNNSLKPCADKSHLLTFPDNGVK 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Db      61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSEKDMNSLSEFCIARDSHLVITDNOEMS 120
Qy      121 LFEYIGDQFYWIGLRNINIGMRWEGSPALSL-RILTNLSIQCGAIHRNGLOASSCEVAL 179
Db      121 LQVFLSEAFQWIGLRNNSGMRWEDGSPINFSRISNSFVQTCGAINKKGLQASSCEVPL 180
Qy      180 QWICKKY 186
Db      181 HGVCKKY 187

RESULT 5
US-10-416-384-1
; Sequence 1, Application US/10416384
; Publication No. US20050260244A1
; GENERAL INFORMATION:
; APPLICANT: University College London
; APPLICANT: GILLESPIE, STEPHEN
; TITLE OF INVENTION: Vaccine Component
; FILE REFERENCE: 068804-0000001
; CURRENT APPLICATION NUMBER: US/10/416,384
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04985
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: G30027433.2
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-416-384-1

Query Match      5.4%; Score 56; DB 6; Length 189;
Best Local Similarity 27.5%; Pred. No. 39;
Matches 19; Conservative 9; Mismatches 35; Indels 6; Gaps 2;

Qy      10 LELPE-APQVQDESRRKALKAVLHRRPLSRFAMVAVLGLTVIILMSLMTQRIICGSKYST 68
Db      30 LELPQIVPAMNEVWRLEVPNHPDAFMTASNAQSDFLVYVNGLAFYRAWLALGVDS- 88
Qy      69 GSHCPSCP1 77
Db      89 ----QACPL 93

RESULT 6
US-10-842-206-40
; Sequence 40, Application US/10842206
; Publication No. US20050256039A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, Jeffrey D
; APPLICANT: Sciore, Paul J
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: Cura 570A
; CURRENT APPLICATION NUMBER: US/10/842,206
; CURRENT FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 40
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-842-206-40

Query Match      4.1%; Score 42; DB 6; Length 188;
Best Local Similarity 28.4%; Pred. No. 1.2e+03;
Matches 19; Conservative 8; Mismatches 28; Indels 12; Gaps 4;

Qy      107 GSHLTFFPDN--QGVR----LFG--EYLQDQFYWIGLRNIDGMRWEG----GPALSLRIL 154
```

```
Db      51 GFHLQILPDGSGVQGRQDHSIFGILFISVAVLGVSIRGVDSGLYLGNMDKGELYSERKL 110
Qy      155 TNSLIQR 161
Db      111 TSECIFF 117

RESULT 7
US-10-980-459-32
; Sequence 32, Application US/10980459
; Publication No. US20050256042A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: ChillaKuru, Rajeev A.
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larocheille, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Nandev, Pradyumna Kumar
; APPLICANT: Valax, Pascal
; APPLICANT: Yim, Zachary
; APPLICANT: Hahne, William
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis
; FILE REFERENCE: Cura-57 AM
; CURRENT APPLICATION NUMBER: US/10/980,459
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 10/435,087
; PRIOR FILING DATE: 2003-5-9
; PRIOR APPLICATION NUMBER: 10/842,179
; PRIOR FILING DATE: 2004-5-10
; PRIOR APPLICATION NUMBER: 60/541,728
; PRIOR FILING DATE: 2004-2-4
; PRIOR APPLICATION NUMBER: 60/545,278
; PRIOR FILING DATE: 2004-2-18
; PRIOR APPLICATION NUMBER: 60/____
; PRIOR FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 32
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-459-32

Query Match      4.1%; Score 42; DB 6; Length 188;
Best Local Similarity 28.4%; Pred. No. 1.2e+03;
Matches 19; Conservative 8; Mismatches 28; Indels 12; Gaps 4;

Qy      107 GSHLTFFPDN--QGVR----LFG--EYLQDQFYWIGLRNIDGMRWEG----GPALSLRIL 154
Db      51 GFHLQILPDGSGVQGRQDHSIFGILFISVAVLGVSIRGVDSGLYLGNMDKGELYSERKL 110
Qy      155 TNSLIQR 161
Db      111 TSECIFF 117

RESULT 8
US-10-945-853-2
; Sequence 2, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Santicola-Nadel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; TITLE OF INVENTION: Cripco-Specific Antibodies
; FILE REFERENCE: BSNALL7CPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
```



```
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 246
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-246
```

```
Query Match          3.9%; Score 40.5; DB 6; Length 189;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 16; Indels 9; Gaps 2;
```

```
QY 113 PPDNGVKLFGEYLGQDFYWG-----LRNIDGWRMEG 146
DB 98 YPTN---NLNDIFGARLWPSBTVAIGLEKLDGKTEYG 134
```

```
RESULT 12
US-10-467-657-2690
/ Sequence 2690, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2690
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2690
```

```
Query Match          3.9%; Score 40.5; DB 6; Length 189;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 16; Indels 9; Gaps 2;
```

```
QY 113 PPDNGVKLFGEYLGQDFYWG-----LRNIDGWRMEG 146
DB 98 YPTN---NLNDIFGARLWPSBTVAIGLEKLDGKTEYG 134
```

```
RESULT 13
US-10-945-853-1
/ Sequence 1, Application US/10945853
/ Publication No. US20050255117A1
/ GENERAL INFORMATION:
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Sanicola-Nadel, Michele
/ APPLICANT: Adkins, Heather
/ APPLICANT: Miklasz, Steven Donald
/ APPLICANT: Rayhorn, Paul
/ APPLICANT: Schiffer, Susan Gail
/ APPLICANT: Williams, Kevin
/ TITLE OF INVENTION: Crip-to-Specific Antibodies
```

```
/ FILE REFERENCE: BGNAL17CPCCN
/ CURRENT APPLICATION NUMBER: US/10/945, 853
/ CURRENT FILING DATE: 2004-09-20
/ PRIOR APPLICATION NUMBER: PCT/US02/31462
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: PCT/US02/11950
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/286,782
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/293,020
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/301,091
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/367,002
/ PRIOR FILING DATE: 2002-03-22
/ NUMBER OF SEQ ID NOS: 9
/ SEQ ID NO 1
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-945-853-1
```

```
Query Match          3.6%; Score 37.5; DB 6; Length 188;
Best Local Similarity 24.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 10; Mismatches 28; Indels 17; Gaps 5;
```

```
QY 19 QDESRWKLKAVLHRRPHLSRFPMVALGLTVMISLMTQRIL---CCGSKDSTC---SHC 72
DB 47 RDDSIVQPEEPAIRRSQ-RVPMG-----IQSKRLNRCC-LNGTCMLGSFC 95
QY 73 PSCPLWTRNGSH 85
DB 96 ACPPSFYGRNCEH 108
```

```
RESULT 14
US-10-821-234-1393
/ Sequence 1393, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1393
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1393
```

```
Query Match          3.6%; Score 37; DB 6; Length 188;
Best Local Similarity 20.0%; Pred. No. 4.2e+03;
Matches 11; Conservative 11; Mismatches 15; Indels 18; Gaps 1;
```

```
QY 16 FOVODESRWKLKAVLHRRP-----LSRFPMVALGLTVMIS 52
DB 24 PDRFDSIKNNRNVSNLLYQTNVLVAAAMISTVGFSPFNMLIGLVVLF 78
```

```
RESULT 15
US-10-528-031-4
/ Sequence 4, Application US/10528031
/ Publication No. US20050262577A1
/ GENERAL INFORMATION:
/ APPLICANT: ORIDIS Biomed Forschungs- und Entwicklungs GmbH
```

Tue Jan 10 09:41:26 2006

us-09-811-367b-3.rapbn

**Page 7**

```

APPLICANT: Guelly, Christian
APPLICANT: Buck, Charles R.
APPLICANT: Zatloukal, Kurt
TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for the
TITLE OF INVENTION: prevention, diagnosis or treatment of liver disorders and epithelial
FILE REFERENCE: Ordis Blomed
CURRENT APPLICATION NUMBER: US/10/528,031
CURRENT FILING DATE: 2005-03-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4
LENGTH: 188
TYPE: prt
ORGANISM: Homo sapiens
US-10-528-031-4

```

Query Match 3.6%; Score 37; DB 6; Length 188;  
Best Local Similarity 20.0%; Pred. No. 4.2e+03;  
Matches 11; Conservative 11; Mismatches 15; Indels 18; Gaps 1.

[illegible]

Search completed: January 9, 2006, 15:56:42  
Job time : 10.6478 secs

THE NEW YORK PUBLIC LIBRARY  
ASTOR LENOX TILDEN FOUNDATION  
1900

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3009 Seconds  
(without alignments)  
988.409 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSYSTLELPAAAPRVQD.....GLHASSCEVALQWICEKVL 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r:80: \*  
2: p1r1: \*  
3: p1r2: \*  
4: p1r3: \*  
5: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	I59421 mast cell function
2	65	6.3	188	2	C86508 hypothetical prote
3	65	6.3	188	2	H72114 transcription regu
4	59.5	5.7	188	2	T33623 hypothetical prote
5	56.5	5.5	189	2	B95865 conserved hypotet
6	56	5.4	189	2	AH1128 acetyltransferase
7	56	5.4	189	2	AC1489 acetyltransferase
8	55.5	5.4	189	2	A95110 acetyltransferase,
9	55	5.3	189	2	E96569 probable IAA6 prot
10	55	5.3	189	2	S58493 auxin-induced prot
11	53.5	5.2	189	2	G97978 conserved hypotet
12	53.5	5.2	189	2	D81564 hypothetical prote
13	53	5.1	189	2	T19559 hypothetical prote
14	52	5.0	188	2	AC1355 methylphosphorites
15	51.5	5.0	188	2	S74560 hypothetical prote
16	49	4.7	188	2	I51347 MHC class I - A2la
17	49	4.7	189	2	B71542 hypothetical prote
18	48.5	4.7	189	2	AH1029 probable membrane
19	48	4.6	188	2	G87336 conserved hypotet
20	48	4.6	189	2	S34632 dnaJ protein homol
21	47.5	4.6	188	2	TC4680 vascular endotheli
22	47.5	4.6	189	2	IVBO11 interferon alpha-1
23	47.5	4.6	189	1	IVBO11 interferon alpha-1
24	47.5	4.6	189	2	B72234 RNA polymerase sig
25	47.5	4.6	189	2	A25556 hypothetical 21.2K
26	47	4.5	189	2	B29795 circumsporozoite p
27	47	4.5	189	2	A90172 conserved hypotet
28	46	4.4	188	2	A34014 integrin alpha-3 c
29	46	4.4	189	2	T02792 hypothetical prote

30	45.5	4.4	188	2	A39787 teratocarcinoma-de
31	45.5	4.4	189	1	IWMSA6 interferon alpha-1
32	45.5	4.4	189	2	I49773 murine interferon
33	45.5	4.4	189	2	S52803 hypothetical prote
34	45	4.3	188	2	S09789 hypothetical prote
35	45	4.3	188	2	C69173 conserved hypotet
36	45	4.3	188	2	B83786 hypothetical prote
37	44.5	4.3	189	1	IVBO1C interferon alpha-1
38	44.5	4.3	189	2	E64527 hypothetical prote
39	44	4.2	188	1	UQ0534 coat protein Ken
40	44	4.2	189	2	T39519 probable signal se
41	44	4.2	189	2	F70125 conserved hypotet
42	44	4.2	189	2	T27306 conserved hypotet
43	44	4.2	189	2	T02821 probable membrane
44	44	4.2	189	2	AG1947 hypothetical prote
45	44	4.2	189	2	A83586 probable transcrip

## ALIGNMENTS

```

RESULT 1
I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A>Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: UNIPROT:Q64335; UNIPARC:UPI0000030101; EMBL:X79812; NID:G1020141; P
C:Genetics:
A:Gene: mafa

Query Match          100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 9.3e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAAPRVQDSDRWKXAVLHRCVSYLVWVALGLTVILMSLLYORTL 60
DB 1 MADNSYSTLELPAAAPRVQDSDRWKXAVLHRCVSYLVWVALGLTVILMSLLYORTL 60
QY 61 CGSGKGFMCSCRCPNLMMRNGSHCYFSMEKRDWNSLKFCADKSHLTFPDNQGVN 120
DB 61 CGSGKGFMCSCRCPNLMMRNGSHCYFSMEKRDWNSLKFCADKSHLTFPDNQGVN 120
QY 121 LFOEYVGDFFWYIGLRIDIGWRWEDGPAISLISNSVYQKGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDFFWYIGLRIDIGWRWEDGPAISLISNSVYQKGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 2
C86508
hypothetical protein y99E (imported) - Chlamydomonas pneumoniae (strain J138)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86508
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86508
A>Status: preliminary
A:Molecule type: DNA

```

A;Residues: 1-188 <STO>  
A;Cross-references: UNIPROT:Q9Z944; UNIPARC:UPI00000D4127; GB:BA000008; NID:g9976512; P  
A;Experimental source: strain J138  
C;Genetics:  
A;Gene: yqgE  
;Superfamily: hypothetical protein H10304

Query Match	6.3%	Score 65;	DB 2;	Length 188;
Best Local Similarity	33.8%	Pred. No. 82;		
Matches	22;	Conservative	6;	Mismatches 33;
			Indels	4;
			Gaps	3;

QY	60	LCCGSGFMQSQCRR--CPNWL-MRNGSHCYESEMEXRD-VNSSLKRCADKDSHLLTEPD	115
Db	124	LCFGSGWAGQLKEKFLSNWFAPLNKDYYFYSEEDLMALVLDLGGKYASLSLTPD	183

Qy	116	NQGVN	120
		:	
Db	184	NLLLN	188

### RESULT 3

```
transcription regulator, probable CP06333 (imported) - Chlamydomonas reinhardtii (strains
C:species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii
C:date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
```

R. Kalkman, S. Mitchell, W. Marathe, R. Lammel, C. Fan, J. Olinger, L. Grimwood, J. Nature Genet. 21, 385-389, 1999

A;Accession: H72114  
A;Molecule type: DNA  
A;Residues: 1-188 <ARN>

A) Experimental source: strain CWL029  
R. Dodson, T. D. Brunham, R. C. Shen, C. J. Gill, S. R. Heidelberg, J. F. White, O. Hickey, C. J. Dodson, R. J. Gilm, M. J. Nelson, W. J. DeBoy, R. J. Kolonay, J. McClarty, G. Salzberg

ATitle: Genome sequences of *Chlamydia trachomatis* MOPn and *Chlamydia pneumoniae* AR39.  
A.Reference number: AB1500; MUID:20150255; PMID:10684935  
A.Accession: E81555

A:Residues: 1-188 (REA)  
A:Cross-references: UNIPARC:UPI00000D4127; GB:AE002221; NID:97189543; PIDN:  
A:Experimental source: strain AR39, HL cells

C:Generics:  
A:Gene: yggE, CP0633  
C:Superfamily: hypochemical protein HI0304

Query Match	6.3%;	Score 65;	DB 2;	Length 188;
Best Local Similarity	33.8%;	Pred. No. 82;		
Matches 22;	Conservative 6;	Mismatches 33;	Indels 4;	Gaps 3

QY 60 LCCGSKGFMCQCSR--CPNLMLMRGSHCYFFSMKCRDWNSSLKRCADKSGHLLTPPD 115  
Db 124 LCFGSGMQAGOLEKEFLSNWFIAGCNKDYFSEEDLWMLVLKLGKRYASLSTYPD 183

QY	116	NOGVN	120
		:	
Db	184	NLLLN	188

## RESULT 4

hypothetical protein F40G9.10 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text change 09-Jul-2004

R:Graves, T.; Sutterer, C.; Ozersky, P.  
submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of C. elegans cosmid F40G9  
A:Reference number: 221378

**A;Accession:** T33623

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-188 <GRA>  
A:Cross-references: UNIPROT:Q9TZ75; UNIPARC:UPI000007BD20; EMBL:AF099919; PIDN:AAC68804.  
A:Experimental source: strain Bristol N2, clone F40G9  
C:Genetics:  
A:Gene: CESP:F40G9.10  
A:Map position: 3  
A:introns: 63/3; 99/1; 113/3; 153/3

Query Match	5.7%	Score 59.5	DB 2	Length 188
Best Local Similarity	24.7%	Pred. No. 2.7e+02		
Matches 22	Conservative 12	Mismatches 30	Indels 25	Gaps 5

QY	7	WMRNGSHCYCYFSEMERDWNLSLKFCADKSGHLL	----	TFPDNQ	-----	GVNLPEQY	125
		:  :  :  :  :  :  :  :  :  :  :  :  :					
Db	54	WFSYTNPCFKSTARAANFNDAHNAKRSSEGLASIS	-----	LSLTENOQFLVOLA	-----	SAAGNRVNSKTY	113
		:  :  :  :  :  :  :  :  :  :  :  :  :					

```

QY      126 VGEDFYWIGL----RDIDGWRWEDGPALS 150
          |||      |  |  |  |  |  |  |  |  |
Db      114 V-----MGLIFENR-----WSWTIDGSSVN 134

```

RESULT 5  
B95865

```
C:\Accession: B95865
C:\Date: 24-Aug-2001 #sequence_rev: 24-Aug-2001 #text_change 09-Jul-2004
C:\Species: Sinorhizobium meliloti
C:\Conserved_hypothetical_protein: (unannotated)
C:\Conserved_hypothetical_protein: meliloti
```

A-Reference number:A95842; PMID:21396508; EMBL:U148141

A/Accession: B93085  
A/Status: preliminary  
A/Molecule type: DNA  
A:Residues: 1-189 <K11

A. C. 10088-References: UNIPROT:Q9ZWM5; UNIPROT:Q9F100UNQ8B466; GB:U0531365; EIDN:U05460366.4.  
 A. C. 10089-Experimental source: strain 1021, megaplasmid p5yMB  
 R. Gailberet, F. J. Finan, T. M. Long, S. R. Pulver, A. J. Abola, P. J. Ampe, F. Barloy-Hubler,  
 J. L. Dubet, J. P. Cowie, A. J. Davies, R. W. Drano, S. Pedersmit, N. A. Fisher, R. F.

L. J. Hyman, R.W. Jones, T. Science 293, 668-672, 2001  
A. Authors: Kahn, D. J. Kahn, M.L. J. Kalman, S. Keating, D.H. J. Kiss, E. Komp, C. J. Lelaure,  
P. Leland, P. Leland, M. Leland, F. J. Wadsworth, D. H. Wallis, D. H. Ward, K. V. Leh, K.

A.Comments: annotation  
 A.Reference number: A96039; WUID:21368234; PMID:11474104  
 A.Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A.Citation:

A;Gene: Smb20186  
A;Genome: plasmid

Best Local Similarity 21.7%; Pred. NO. 5.1e+02;  
Matches 31; Conservative 15; Mismatches 54; Indels 43; Gaps 6

Db  
28 CASNVTVRIGSGTA-----HNHAGC-----CTKC-----WKEGALFAQIAYVVG 67

Db 68 RD-NVNVTSGAELKLVDPESATIQRYACRDCGTHM-----GRIENTGHFFYGLDFVHTEL 122

123 SDETGWSPPPEFAAFVSSIIESGV 145

RESULT 6  
AH1126  
acetyltransferase homolog [mc0431 (imported)] - *Listeria monocytogenes* (strain EGD-e)

C;Species: *Listeria monocytogenes*



C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AH1128  
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Kretz, U.  
Science 294, 849-852, 2001  
A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*.  
A/Reference number: AB1077; MUID:21537279; PMID:1167669  
A/Accession: AH1128  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-189 <GLA>  
A/Cross-references: UNIPROT:Q8Y9T9; UNIPARC:UPI0000054ESC; GB:NC\_003210; PIDN:CAC98510.1  
A/Experimental source: strain EGD-e  
C/Genetics:  
A/Gene: lmo0431  
C/Superfamily: galactoside acetyltransferase

Query Match 5.4%; Score 56; DB 2; Length 189;  
Best Local Similarity 31.5%; Pred. No. 5.7e+02;  
Matches 28; Conservative 8; Mismatches 33; Indels 20; Gaps 5;

QY 99 SLKFCADKGSLLTFPPDNGVNLFOEYVGEDFYWIGLRIDGKRWED---GPALSLTL 154  
DB 68 SLPEYSDFGKH-ITFGKNIFINLVTFV-----DLGGITIEDNVLIQPGALVTV 116  
117 NMLVSPK---KRRGLRVAPICVKNAMI 141

RESULT 7  
AC1489  
acetyltransferase homolog lin0451 [imported] - *Listeria innocua* (strain Clp11262)  
C/Species: *Listeria innocua*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AC1489  
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Kretz, U.  
Science 294, 849-852, 2001  
A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*.  
A/Reference number: AB1077; MUID:21537279; PMID:1167669  
A/Accession: AC1489  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-189 <GLA>  
A/Cross-references: UNIPROT:Q92E8K; UNIPARC:UPI000000CC232; GB:AL592022; PIDN:CAC95603.1  
A/Experimental source: strain Clp11262  
C/Genetics:  
A/Gene: lin0451  
C/Superfamily: galactoside acetyltransferase

Query Match 5.4%; Score 56; DB 2; Length 189;  
Best Local Similarity 31.5%; Pred. No. 5.7e+02;  
Matches 28; Conservative 8; Mismatches 33; Indels 20; Gaps 5;

QY 99 SLKFCADKGSLLTFPPDNGVNLFOEYVGEDFYWIGLRIDGKRWED---GPALSLTL 154  
DB 68 SLPEYSDFGKH-ITFGKNIFINLVTFV-----DLGGITIEDNVLIQPGALVTV 116  
117 NMLVSPK---KRRGLRVAPICVKNAMI 141

RESULT 8  
A95110  
acetyltransferase, GNAT family [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C/Species: *Streptococcus pneumoniae*  
C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 31-Dec-2004  
C/Accession: A95110  
R/Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heik on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple, nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.  
A/Reference number: A95000; MUID:21357209; PMID:11463916  
A/Accession: A95110  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-189 <KIR>  
A/Cross-references: UNIPROT:Q97876; UNIPARC:UPI0000051661; GB:AE005672; PIDN:AAK75074.1  
A/Experimental source: strain TIGR4  
C/Genetics:  
A/Gene: SP0953  
C/Superfamily: ribosomal protein serine N-acetyltransferase

Query Match 5.4%; Score 55.5; DB 2; Length 189;  
Best Local Similarity 24.0%; Pred. No. 6.4e+02;  
Matches 23; Conservative 14; Mismatches 36; Indels 23; Gaps 4;

QY 95 DNSSLKFCADKGSLLTFPPDNGV-----NLFOEYVGEDFYWIGLRIDGKRWEDGPAL 149  
DB 28 DDAEAFDASDGNKRRYRFPNOSLEETKNIAQYLANPL-----GRW----- 71  
150 SLILSNVQKCGTIRHCGH-ASSCEVALQWI 182  
QY 72 GIEIKSNG--QFTGIDHKKIDSVLKAAGIYINK 105

RESULT 9  
E96569  
probable IAA6 protein, 42631-41742 [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: E96569  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: E96569  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-189 <STO>  
A/Cross-references: UNIPROT:Q38824; UNIPARC:UPI0000126696; GB:AE005173; NID:G6862944; P  
A/Experimental source: auxin-induced protein aux28  
C/Genetics:  
A/Gene: P14G24.10  
A/Map position: 1  
C/Superfamily: auxin-induced protein aux28

Query Match 5.3%; Score 55; DB 2; Length 189;  
Best Local Similarity 25.2%; Pred. No. 7.1e+02;  
Matches 28; Conservative 16; Mismatches 43; Indels 24; Gaps 5;

QY 3 DNGISTLELPAPRVODDSRMVKAVLHRCVSYL-----VMVALGLITVILMSLL 55  
DB 52 ENSVSVSVEBSLPV-----KSQAVGMPVPSYRKKNKNERASAIGVVKV-SMDGVP 104  
QY 56 YORTLCCGSKGFMCSQCRCPNLM-----MENGSHCYT---FSMEKRW 96  
DB 105 YMRKIDGSSNSYINLVTVLENTFGCIGIGVAKGKKCEYIIITYEDKRD 155







GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 96.4956 Seconds  
(without alignment)  
1374.564 Million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036  
Sequence: 1 MADNSISTLELPAPRVOD.....GLHASSCEVALQWICEKILP 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	Q64335_RAT
2	838	80.9	188	2	O88713_MOUSE
3	545.5	52.7	189	2	O75613_HUMAN
4	525.5	50.7	189	2	O43198_HUMAN
5	164.5	15.9	188	2	O62Y73_CHICK
6	164.5	15.9	188	2	O62Y76_CHICK
7	159.5	15.4	188	1	CLC51_HUMAN
8	159.5	15.4	188	2	O52M11_HUMAN
9	134	12.9	189	2	O61969_MOUSE
10	121	11.7	189	2	O8C634_MOUSE
11	92.5	8.9	188	2	O9W012_DROME
12	87	8.4	189	2	O96D89_HUMAN
13	85.5	8.3	189	2	O60S03_CAEER
14	75.5	7.3	188	2	O9W3D8_DROME
15	73	7.0	189	2	O18202_CAEEL
16	69	6.7	188	2	O84RL2_ARATH
17	66.5	6.4	188	2	O4UHL7_TREAN
18	65	6.3	188	1	Y139_CHLUPN
19	62.5	6.0	188	2	O7Q249_ANOGA
20	61.5	5.9	188	2	O7K7K8_CAEEL
21	60.5	5.8	189	2	O86L29_MYTEO
22	60	5.8	188	2	O9DVM3_SHIV1
23	59.5	5.7	188	2	O4IE26_GIBZE
24	59.5	5.7	188	2	O9TZ75_CAEEL
25	59	5.7	188	2	O8Q3K3_SHIV1
26	58.5	5.6	188	2	O68P15_CENSC
27	57	5.5	189	2	O5LSN9_CHLAB
28	56.5	5.5	188	2	O9HFA9_9HETE
29	56.5	5.5	189	1	GFA_RHIME
30	56	5.4	189	2	O723NO_LISMF
31	56	5.4	189	2	O8Y9T9_LISMO

32	56	5.4	189	2	O92EK8_LISIN	O92EK8 listeria in
33	55.5	5.4	188	2	O5D9G7_SCHJA	O5D9G7 schistosoma
34	55.5	5.4	189	2	O97R76_STRPN	O97R76 streptococc
35	55	5.3	189	1	IAA6_ARATH	O38824 arabidopsis
36	55	5.3	189	2	O8A4T4_BACTN	O8A4T4 bacteroides
37	54.5	5.3	189	2	O7OR55_SHIV1	O7OR55 human immun
38	54.5	5.3	189	2	O7ZH46_SHIV1	O7ZH46 human immun
39	54.5	5.3	189	2	O7ZH59_SHIV1	O7ZH59 human immun
40	54	5.2	189	1	Y630_CHLCPV	O822P9 chlamydophi
41	54	5.2	189	2	O75J03_DICDI	O75J03 dictyosteli
42	54	5.2	189	2	O4Y05_CORUK	O4Y05 corynebacte
43	54	5.2	189	2	O6IXP3_SHIV1	O6IXP3 human immun
44	53.5	5.2	188	2	O8DB05_VIBVU	O8DB05 vibrio vuln
45	53.5	5.2	189	2	O9K250_CHLUPN	O9K250 chlamydia p

## ALIGNMENTS

## RESULT 1

Q64335\_RAT PRELIMINARY; PRT; 188 AA.

ID Q64335\_RAT

AC Q64335; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-FEB-2005 (TREMBLrel. 29, last annotation update)

MAFA protein (mast cell function associated antigen).

GN Name=Kilg1; Synonyms=MAFA, mata;

OC Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.

OC NCBI\_TaxID=10116;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Sprague Dawley; TISSUE=Testis;

RX MEDLINE=97240766; PubMed=9120279;

RA Bocsk J P., Gutmann M D., Pecht I.;

RT "Analysis of the gene encoding the mast cell function-associated

antigen and its alternatively spliced transcripts.";

RL J. Immunol. 158:3235-3243(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96016176; PubMed=7568140;

RA Gutmann M.D., Tal M., Pecht I.;

RT "A secretory inhibitory signal transduction molecule on mast cells is

another C-type lectin.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

DR EMBL; X97191; CAA65829.1; -; Genomic\_DNA.

DR EMBL; X79812; CAA65208.1; -; mRNA.

DR EMBL; X97192; CAA65829.1; JOINED; Genomic\_DNA.

DR EMBL; X97193; CAA65829.1; JOINED; Genomic\_DNA.

DR EMBL; X97194; CAA65829.1; JOINED; Genomic\_DNA.

DR EMBL; X97195; CAA65829.1; JOINED; Genomic\_DNA.

DR PIR; I59421; I59421.

DR HSSP; P26718; IKCG.

DR EMBL; ENSRNOG0000014918; Rattus norvegicus.

DR RGD; 61978; K191.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR001304; Lectin\_C.

DR Pfam; PF00059; Lectin\_C\_1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PSS0041; C-TYPE\_HECTIN\_2; 1.

DR SEQUENCE 188 AA; 23356 MW; 2CC8032D4D020B15 CRC64;

Query Match 100.0%; Score 1036; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 2; 1e-92;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MADNSISTLELPAPRVODDSRWKVAVLRPCVSYLVNVALGLTVILMSLLYORTL 60
Db	1	MADNSISTLELPAPRVODDSRWKVAVLRPCVSYLVNVALGLTVILMSLLYORTL 60

QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVN 120  
DB 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVN 120  
QY 121 LFOEYVGEDEFWYIGLRIDGWRWEDGPAALSTLSNSVYVCGCTIHRGGLHASSCEVALQ 180  
DB 121 LFOEYVGEDEFWYIGLRIDGWRWEDGPAALSTLSNSVYVCGCTIHRGGLHASSCEVALQ 180  
QY 181 WICEKVL 188  
DB 181 WICEKVL 188

## RESULT 2

088713\_MOUSE PRELIMINARY; PRT; 188 AA.

ID 088713\_MOUSE PRELIMINARY; PRT; 188 AA.  
AC 088713,  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Mast cell function-associated antigen 2F1 (Killer cell lectin-like receptor G1) (MAFA).  
GN Name=KIRG1; Synonyms=Mafa, mafa;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C.B-17 SCID;  
RX MEDLINE=99077194; PubMed=9862378;  
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;  
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-associated antigen', is a lectin-like type II transmembrane receptor expressed by natural killer cells."  
RT Eur. J. Immunol. 28:4409-4417(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SvEvTAcFBr; TISSUE=Spleen;  
RX MEDLINE=99077501; PubMed=9862665;  
RA Blaier C., Kaufmann M., Picher H.;  
RT "Virus-activated CD8 T cells and lymphokine-activated NK cells express the mast cell function-associated antigen MAFA, an inhibitory C-type lectin."  
RT J. Immunol. 161:6451-6454(1998).  
RL EMBL; AF097357; AAD03718.1; -; mRNA.  
DR EMBL; AF317727; AAK4082.1; -; Genomic DNA.  
DR EMBL; AJ010751; CAA09342.1; -; mRNA.  
DR HSSP; Q13241; 1B6E.  
DR Ensembl; ENSMUSG0000030114; Mus musculus.  
MG1; MG1:1355294; KIRG1.  
DR GO; GO:0016021; C:Integral to membrane; TAS.  
DR GO; GO:0005529; F:sugar binding; TAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLCCT; 1.  
DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
DR Lectin; Receptor.  
FT CHAIN 2 188  
FT SEQUENCE 188 AA, 21396 MW, 876336802E1134F1 CRC64;  
Query Match 80.9%; Score 838; DB 2; Length 188;

Beat Local Similarity 80.7%; Pred. No. 3.6e-73;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPCVSYLWVALGLITVILMSLLYQRTL 60  
DB 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPHISRAMVALGLITVILMSLLMYQIL 60  
QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVN 120  
DB 61 CCGSKDSTCHSCPILMTNRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVK 120  
QY 121 LFOEYVGEDEFWYIGLRIDGWRWEDGPAALSTLSNSVYVCGCTIHRGGLHASSCEVALQ 180  
DB 121 LFGETLQDFYWIGLRIDGWRWEGPALSILRLITLSLORCGAIHRNGLAASCEVALQ 180  
QY 181 WICEKVL 187  
DB 181 WICEKVL 187

## RESULT 3

075613\_HUMAN PRELIMINARY; PRT; 189 AA.

ID 075613\_HUMAN PRELIMINARY; PRT; 189 AA.  
AC 075613;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE ITIM-containing receptor MAFA-L (Mast cell function-associated antigen homolog).  
GN Name=MAFA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99057052; PubMed=9842918;  
RX DOI=10.1002/(SICI)1521-4141(199811)28:11<3755::AID-IMMU3755>3.0.CO;2-3;  
RA Butcher S., Arney K.L., Cook G.P.;  
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene complex and expressed by basophils and NK cells."  
RT Eur. J. Immunol. 28:3755-3762(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99077194; PubMed=9862378;  
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;  
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-associated antigen', is a lectin-like type II transmembrane receptor expressed by natural killer cells."  
RT Eur. J. Immunol. 28:4409-4417(1998).  
RL EMBL; AF081675; AAC32200.1; -; mRNA.  
DR EMBL; AF097358; AAD03719.1; -; mRNA.  
DR HSSP; Q13241; 1B6E.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLCCT; 1.  
DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
DR KIR Receptor.  
FT SEQUENCE 189 AA, 21206 MW, FA9023F1523656A8 CRC64;

Query Match 52.7%; Score 545.5; DB 2; Length 189;

Beat Local Similarity 55.1%; Pred. No. 9.3e-45;  
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPCVSYLWVALGLITVILMSLLYQRTL 60  
DB 1 MTDYSIVYMLELPRTAQNDYGPQKSSSSRSCCVATALGLITVILSVLLYQWIL 60  
QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVN 120  
DB 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSSLKFCADKGSHTLTFPDNGVN 120

Db 6 CQSSNNSTCASCSPCDRMMKXGNHCYFVSVEKQDNSSLFECFLARDSHLLIVITDQEMS 120  
 Qy 121 LPEQVEEDPEYTWGLGLRIDGSMREDSPALSLSLNSVQCKGTHRCGLHAASCEVAL 179  
 Db 121 LLOVFLSEAFCHGLGLNNSGMRWEDSPANFSRISNSFVQTCGAINNGQASCEVPL 180  
 Qy 180 QWICEKY 186  
 Db 181 HWVCKKV 187

```

RESULT 4
043198_HUMAN
ID   O43198_HUMAN PRELIMINARY;          PRT;   189 AA.
AC   O43198;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mast cell function-associated antigen.
GN   Name=MAFA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC   Homo.
NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Enzyme digested lung;
RX   MEDLINE=98438735; PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;
RA   Lamers M.B., Lamont A.G., Williams D.H.;
RT   "Human MAFa has alternatively spliced variants.";
RL   Biochim. Biophys. Acta 1399:209-212(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Enzyme digested lung;
RA   Lamers M.B.A.C., Lamont A.G., Williams D.H.;
RT   Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF034952; AAC34731.1; -; mRNA.
DR   HSSP; I13241; 1B6E.
DR   GO; GO:0016021; C:Integral to membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0005529; F:sugar binding; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR   GO; GO:0006968; P:cellular defense response; TAS.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   189 AA;  21079 MW;  15E042AD40B2B4F6 CRC64;

```

[illegible]

06ZYP3 CHICK  
ID 06ZYP3 CHICK PRELIMINARY; PRT; 188 AA.  
AC 06ZYP3;  
DT 05-JUL-2004 (TREMBLREL. 27, Created)  
DT 05-JUL-2004 (TREMBLREL. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLREL. 27, Last annotation update)  
DE B-1ec protein.  
GN Name=B-1ec;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Bursa;  
RX PubMed=15749683;  
RA Rogers S.L., Gobel T.W., Vierlboeck B.C., Milne S., Beck S.,  
RA Kaufman J.J.,  
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec  
RT reveals that the NK Complex and the MHC share a common ancestral  
RT region.";  
RL J. Immunol. 174:3475-3483(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Bursa;  
RA Rogers S.L.;  
RT "Characterisation of C-type lectin-like receptors in the chicken  
RT MHC.";  
RL Thesis (2002). Department of Pathology and Microbiology, University of  
RL Bristol, Bristol, United Kingdom.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Bursa;  
RA Kaufman J.F.;  
RL EMBL: AJ634337; CAG25421.1; -; mRNA.  
DR EMBL: AJ634337; CAG25421.1; -; mRNA.  
DR HSRP: Q9H8P0. 1x93.  
DR GO: GO:0005528, F: sugar binding; IEA.  
DR InterPro: IPR002353; Antifreeze1.  
DR InterPro: IPR001304; Lectin\_C.  
DR Pfam: PF00059; Lectin\_C\_1.  
DR PRINTS: PR00356; ANTIFREEZE1.  
DR SMART: SM00034; CLECT. 1.  
DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; UNKNOWN\_1.  
DR PROSITE: PS00615; C\_TYPE\_LECTIN\_2; 1.  
SQ SEQUENCE 188 AA; 2105 MW; 6A55AC3C9B587440 CRC64;

[illegible]

```

GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RX PubMed=15749883;
RA Rogers S.L., Gobel T.W., Vierterboeck B.C., Milne S., Beck S.,
RA Kautman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RX Rogers S.L.;
RA "Characterisation of C-type lectin-like receptors in the chicken
RA MHC.";
RT Theiss (2002), Department of Pathology and Microbiology, University of
RT Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RA Kautman J.F.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ634334; CAG25418.1; -; mRNA.
DR HSP; O9H8F0; 1K9J.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro: IPR002353; Antifreeze1.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTI-FREEZE1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SO SEQUENCE 188 AA; 20957 MW; 3FDSBD9DBF9FE41 CRC64;

Query Match 15.9%; Score 164.5; DB 2; Length 188;
Best Local Similarity 24.5%; Pred. No. 9.4e-08;
Matches 39; Conservative 32; Mismatches 71; Indels 17; Gaps 6;

QY 34 CYSYLVMAVAGLITVIMSLLYQRTLCGSGKGF--CGQRCRCPMLMRNSHCYPSM 91
DB 26 CVTFOITMA-AVFTVILLITAVAF-----AVQAFQHPQCAQCPEPDWIGFRGKCYFSE 78
QY 92 EKRDNNSLTKFCADKSHLTFPPDNGVNLFOEYVGEDFYWIGLR---DIDGMRMEDGPA 148
DB 79 DESNNTSSQNNKSGALGASLAVDSADLSFTYRHKSSPHWVGLSREGKEHMEWVNRSP 138

QY 149 IS--LSISNSVYVQCGTTRCGLASGCEVALQWICEK 185
DB 139 LSHLFOVQGDGL---CAVLGDAGLSSSHCSARRNWCTK 174

RESULT 7
ID CLC5A HUMAN STANDARD; PRT; 188 AA.
AC Q9NY25; O9UK00;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type lectin domain family 5 member A (C-type lectin superfamily
DE member 5) (Myeloid DAP12-associated lectin) (MDL-1).
GN Name=CLC5A; Synonyms=CLEC5A, MDL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,
RP INTERACTION WITH TYROBP, AND MUTAGENESIS OF LYS-16.
RX MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;
RA Baker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
RT "Myeloid DAP12-associated lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RA Mueller A., Merz H., Feller A.C.;
RT "Expression of MDL-1 in human blood and cell lines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vandbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strommatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speith J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohltmann F.E., Cook L.L.,
RA Hickenotheam M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen B.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Sims E., Levy R., Clendenning T., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flick P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
RN [4]
RP FUNCTION: May be involved in proinflammatory activation of myeloid
RP cells via TYROBP-mediated signaling in a calcium-dependent manner.
CC [1] SUBUNIT: Interacts with TYROBP.
CC [2] TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in
CC cell lines of other origins. Expression is down-regulated when
CC monocytes differentiate into dendritic cells.
CC [3] SIMILARITY: Contains 1 C-type lectin domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF139768; AAF02491.1; -; mRNA.
CC EMBL; AJ271684; CAB71334.1; -; mRNA.
CC EMBL; AC073647; AAS07444.1; -; genomic DNA.
CC HSP; P22897; IE6G.
CC Ensembl; ENSG00000090269; Homo sapiens.
CC HGNC; HGNC:2054; CLC5A.
CC MIM; 604987; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005488; F: binding; TAS.
CC GO; GO:0006988; P: cellular defense response; TAS.
CC GO; GO:0007165; P: signal transduction; TAS.
CC InterPro; IPR002353; Antifreeze1.

```



DR Interpro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 DR Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 DR Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=lung and heart;  
 RG NIH MGC Project;  
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC093714; AAH93714.1; -; mRNA.  
 KW Lectin.  
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
 Query Match 15.4%; Score 159.5; DB 1; Length 188;  
 Best Local Similarity 25.5%; Pred. No. 2.9e-07;  
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;  
 QY 40 MWALGLTVTL---MSLL-----YQRTLCGS-----XGFMCS 70  
 DB 5 MITSGLIVVLLKVGWTLFLYLPQIFNKNDGFTTTSYGVQIFGSSSPSPNGFIT 64  
 QY 71 QC--SRCPNLMNRNGSHCYFMSKRDWNSLKFCADKGSHTLTPDNGVNLFOEYVS 128  
 DB 65 RSYGVCPDMEFYQARCFPLSTSSSWNSRDFCKGKSTLAIVTPKTLFLDITDA 124  
 QY 129 DPYWGTL---RDIDGRWEDGALSLISLNSVQKCGTHRCGL---HASSCEVALQW 181  
 DB 125 EKYFGLIYHREKRWRWINSVFNQVNTQNFNCAT---GLTKTFDAASCDISYR 181  
 QY 182 ICEK 185  
 DB 182 ICEK 185  
 RESULT 8  
 ID Q52M11 HUMAN PRELIMINARY; PRT; 188 AA.  
 AC Q52M11;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DE C-type lectin, superfamily member 5.  
 GN Name=CLECSA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=lung and heart;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=lung and heart;  
 RG NIH MGC Project;  
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC093714; AAH93714.1; -; mRNA.  
 KW Lectin.  
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;  
 Query Match 15.4%; Score 159.5; DB 2; Length 188;  
 Best Local Similarity 25.5%; Pred. No. 2.9e-07;  
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;  
 QY 40 MWALGLTVTL---MSLL-----YQRTLCGS-----XGFMCS 70  
 DB 5 MITSGLIVVLLKVGWTLFLYLPQIFNKNDGFTTTSYGVQIFGSSSPSPNGFIT 64  
 QY 71 QC--SRCPNLMNRNGSHCYFMSKRDWNSLKFCADKGSHTLTPDNGVNLFOEYVS 128  
 DB 65 RSYGVCPDMEFYQARCFPLSTSSSWNSRDFCKGKSTLAIVTPKTLFLDITDA 124  
 QY 129 DPYWGTL---RDIDGRWEDGALSLISLNSVQKCGTHRCGL---HASSCEVALQW 181  
 DB 125 EKYFGLIYHREKRWRWINSVFNQVNTQNFNCAT---GLTKTFDAASCDISYR 181  
 QY 182 ICEK 185  
 DB 182 ICEK 185  
 RESULT 9  
 ID Q61969 MOUSE PRELIMINARY; PRT; 189 AA.  
 AC Q61969;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Natural killer cell receptor-PI (Fragment).  
 GN Name=NKR-PI 34;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murine; Mus.  
 NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=9238663; PubMed=1517565;  
 RA Giorda R., Weisberg E.P., Ip T.K., Trucco M.;  
 RT "Genomic structure and strain-specific expression of the natural  
 RT killer cell receptor NKR-PI."  
 RL J. Immunol. 149:1957-1963 (1992).  
 DR EMBL; X64719; CAA45972.1; -; mRNA.  
 DR HSSP; 007108; 1FMS.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR Interpro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PSS0041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1



RA Hopkings R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Boeck S.A., Medwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Maira W.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RA NUCLEOTIDE SEQUENCE.  
RA TISSUE=Testis;  
RA Director MGC Project;  
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC076635; BAC36425.1; -; mRNA.  
DR EMBL: BC089473; AAH89473.1; -; mRNA.  
DR ENSEMBL: ENSMUSG00000047720; Mus musculus.  
DR MGI: MGI:2685920; 4922502D21Rik.  
DR GO: GO:0005529; F: sugar binding; IRA.  
DR InterPro: IPR001304; Lectin\_C.  
DR Pfam: PF00059; Lectin\_C; 1.  
DR SMART: SM00034; CLECT\_1.  
DR PROSITE: PS50041; C-TYPE\_LLECTIN\_2; 1.  
DR Hypothetical protein; Lectin.  
SQ SEQUENCE 189 AA; 22107 MW; 2EE5673DBAC2B39E CRC64;  
  
Query Match 11.7%; Score 121; DB 2; Length 189;  
Best Local Similarity 23.4%; Pred. No. 0.0016;  
Matches 36; Conservative 31; Mismatches 69; Indels 18; Gaps 7;  
  
QY 44 GLTITILMSLLAYOR--TLCCSGSGFMC--SQCSRCPETLMRNGSHCYFPMERKDNNSI 100  
DB 37 GAAVALMGFSFPKRTVTRAKNTKDCDEVLCPEDMKLQNCFSRIQHNSMLTAN 96  
QY 101 KFCADKSHLLTFPPDNGVNLFOEYVGE-DFYWIGL-RDIDG-WRNEDGPAISLISLN 156  
DB 97 DTEELMDATLAVFDKTEVEILNMNQIDEMTYWIGLHRQMLGIWWTNSKY-----N 150  
  
QY 157 SVVQ-----KCGTTHRCGLHASSCEVALQWICEK 185  
DB 151 NLHEIDPHGQCAFVHQKIDSTSCEDQKEPCTR 184  
  
RESULT 11  
Q9W012\_DROME PRELIMINARY; PRT; 188 AA.  
ID Q9W012\_DROME PRELIMINARY; PRT; 188 AA.  
AC Q9W012;  
DT 01-MAY-2000 (TREMBLrel.13, Created)  
DT 10-MAY-2000 (TREMBLrel.13, Last sequence update)  
DT 10-MAY-2000 (TREMBLrel.30, Last annotation update)  
DE CG9134-PA, isoform A (CG9134-PC, isoform C) (R615268p).  
GN ORFNames=CG9134;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OC NCBI\_TaxId=7227;  
OX NCBI\_TaxId=7227;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adame M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Anagnostou P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan D.A., Bouck J., Brokstein P., Brotter P.,  
RA Burris K.C., Busam M.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durkin K.D., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jafali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasok P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J.P., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,  
RA Palazolo M., Pittman G.S., Pan S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
Science 287:2185-2195(2000).  
RL Science 287:2185-2195(2000).  
RN [2]  
RA NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537573;  
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Paclel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
melanogaster euchromatic genome sequence";  
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RA NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskaas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celinker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomics perspective";  
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RA NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,  
RA Smith C.D., Tuzy J.L., Whitfield E.J., Bayraktoglu L., Berman B.P.,  
RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review";  
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RA NUCLEOTIDE SEQUENCE.  
RP Berkeley Drosophila Genome Project;  
RG Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Paclel J., Park S., Svirskaas R., Smith E.,  
RA Yu C., Rubin G.;



OY 178 ALQWICE 184  
DB 178 LRPVCO 184

RESULT 14  
Q9W3D8 DROME  
ID Q9W3D8 DROME PRELIMINARY; PRT; 188 AA.  
AC Q9W3D8;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2005 (T-EMBLrel. 13, Last sequence update)  
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)  
DE CG12111-PA (At17652p).  
GN ORFNames=CG12111;  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abri1 J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Baillet R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foutel C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gettel J.H., Gu Z., Guan P., Harris M.,  
RA Haritz N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijzerman C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mlehnha N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spletter E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
RA Svayrtbas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195 (2000).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=2242605; PubMed=12537568;  
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svayrtbas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
[3]

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svayrtbas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomic perspective."  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22426069; PubMed=12537572;  
RX Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review."  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RG Berkeley Drosophila Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacle J., Park S., Svayrtbas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RP FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
[7]  
RN NUCLEOTIDE SEQUENCE.  
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo C.J., Pacle J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB003444; AAP46391.1; -; Genomic\_DNA.  
DR EMBL; AY070795; AAL48417.1; -; mRNA.  
DR HSSP; P35247; 1B08.  
DR Ensembl; CG12111; Drosophila melanogaster.  
DR FlyBase; FBgn0030050; CG12111.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PSS0041; C TYPE LECTIN 2; 1.  
DR SEQUENCE 188 AA; 21771 MW; 8696868CAED1B513A CRC64;  
[8]  
Query Match 7.3%; Score 75.5; DB 2; Length 188;  
Best Local Similarity 20.6%; Pred. No. 42;  
Matches 28; Conservative 27; Mismatches 50; Indels 31; Gaps 9;  
[9]  
OY 132 WIGLRI--DG---WR-----WEDGPALSLSLNSVYOKCTTH---RCGLHA 172  
DB 48 FVRIGDNYTYIETPMKNKNWQAGACGMNAHLASIEDKREMEALIKYMAKGFKNNDYF 107  
OY 79 WMRNGSHCYFYS-MEKRDWNSLKFCAKDSHLLTPPDNGVNI,FOBYV-----GEDEFY 131  
DB 48 FVRIGDNYTYIETPMKNKNWQAGACGMNAHLASIEDKREMEALIKYMAKGFKNNDYF 107  
OY 108 WISGNDIGTGAGAFWMSNGRPMTYAPW-NGPKQMPDNYGN--ENC--VHMFATREMIND 162  
OY 173 SSCCEVALQWICENTLP 188  
DB 163 ANCKIQMLVYCEATEP 178

RESULT 15  
018202\_CAEEL



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Comugen Ltd.

OM protein - protein search, using SW model

Run on: January 9, 2006, 15:25:12 ; Search time 25.2885 Seconds  
(without alignments)  
614.628 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSYSTLELPAPRVQD.....GLHSSCEVALQWICKVLP 188

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5.COMB.pep.\*
- 2: /cgn2\_6/prodata/1/1aa/6.COMB.pep.\*
- 3: /cgn2\_6/prodata/1/1aa/H.COMB.pep.\*
- 4: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep.\*
- 5: /cgn2\_6/prodata/1/1aa/RE.COMB.pep.\*
- 6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	US-08-722-126A-5
2	1036	100.0	188	4	PCT-US95-04258-5
3	54	5.2	189	2	US-09-270-767-31816
4	54	5.2	189	2	US-09-270-767-47033
5	53.5	5.2	189	2	US-09-198-452A-1169
6	50.5	4.9	188	2	US-09-438-185A-761
7	50	4.8	188	2	US-09-270-767-42805
8	47.5	4.6	188	1	US-08-469-427A-5
9	47.5	4.6	188	1	US-08-609-443B-5
10	47.5	4.6	188	1	US-08-569-063C-5
11	47.5	4.6	188	2	US-08-851-896-5
12	47.5	4.6	188	2	US-09-252-991A-29925
13	47.5	4.6	188	2	US-09-107-433-5087
14	47.5	4.6	188	2	US-09-198-452A-135
15	47	4.5	188	2	US-09-543-681A-7232
16	45.5	4.4	188	1	US-07-749-001-5
17	45.5	4.4	188	1	US-08-154-198-5
18	45.5	4.4	188	1	US-08-463-135-5
19	45.5	4.4	188	1	US-08-464-023A-5
20	45.5	4.4	189	2	US-09-902-540-14285
21	44.5	4.3	189	2	US-09-482-273-107
22	44	4.2	188	2	US-09-134-000C-6806
23	44	4.2	188	2	US-09-248-796A-18895
24	44	4.2	189	2	US-09-270-767-35760
25	44	4.2	189	2	US-09-270-767-50997
26	43.5	4.2	188	2	US-09-270-767-58978
27	43.5	4.2	188	2	US-09-605-703B-1580

28	43	4.2	188	2	US-09-134-000C-3652	Sequence 3652, Ap
29	42.5	4.1	188	2	US-09-393-627B-19	Sequence 19, Appl
30	42.5	4.1	188	2	US-09-438-185A-957	Sequence 957, App
31	42.5	4.1	189	2	US-09-902-540-10384	Sequence 10384, A
32	42	4.1	188	2	US-09-122-443-14	Sequence 14, Appl
33	42	4.1	188	2	US-09-558-089-14	Sequence 14, Appl
34	42	4.1	188	2	US-09-558-087-14	Sequence 14, Appl
35	42	4.1	188	2	US-09-248-796A-20257	Sequence 20257, A
36	42	4.1	188	2	US-09-558-474-14	Sequence 14, Appl
37	42	4.1	189	2	US-09-489-038A-11266	Sequence 11266, A
38	42	4.1	189	2	US-09-248-796A-20999	Sequence 20999, A
39	41.5	4.0	188	1	US-08-142-449B-14	Sequence 14, Appl
40	41.5	4.0	189	2	US-08-026-758-1	Sequence 7, Appl
41	41.5	4.0	189	2	US-09-908-594-7	Sequence 7, Appl
42	41.5	4.0	189	2	US-08-469-427A-11	Sequence 11, Appl
43	41	4.0	188	1	US-08-609-443B-11	Sequence 11, Appl
44	41	4.0	188	1	US-08-569-063C-11	Sequence 11, Appl
45	41	4.0	188	1	US-08-569-063C-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-722-126A-5  
Sequence 5, Application US/08722126A  
Patent No. 6034227  
GENERAL INFORMATION:  
APPLICANT: PECHT, Israel  
APPLICANT: GUTTMANN, Marcelo D.  
APPLICANT: TAL, Michael  
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,126A  
FILING DATE: 08-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: PCT/US95/04258  
APPLICATION NUMBER: PCT/US95/04258  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 109257  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: PECHT=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-722-126A-5  
Query Match 100.0%; Score 1036; DB 2; Length 188;  
Best Local Similarity 100.0%; Pred. No. 4, 8e-105;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAAPRVODDSRMKVKAVLHRCVSYLWVALGLTITVILMSLLYORTL 60  
DB 1 MADNSIYSTLELPAAPRVODDSRMKVKAVLHRCVSYLWVALGLTITVILMSLLYORTL 60

QY 61 CCGSKGFMCSQCSRCPNLMNRGSHCYF5MEKRDWNSLKFCAKGSHTLTFPNQGVN 120  
DB 61 CCGSKGFMCSQCSRCPNLMNRGSHCYF5MEKRDWNSLKFCAKGSHTLTFPNQGVN 120

QY 121 LFOEYVGEDFWYIGLRDIDGRWEDGPAISLSISNSVYQCGTTHRCGLHASSCEVALQ 180  
DB 121 LFOEYVGEDFWYIGLRDIDGRWEDGPAISLSISNSVYQCGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVLTP 188  
DB 181 WICEKVLTP 188

RESULT 2  
PCT-US95-04258-5  
; Sequence 5, Application PC/TUS9504258  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NETMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109257  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: PCHT=1 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 188 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-04258-5

Query Match 100.0%; Score 1036; DB 4; Length 188;  
Best Local Similarity 100.0%; Pred. No. 4.8e+105;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LFOEYVGEDFWYIGLRDIDGRWEDGPAISLSISNSVYQCGTTHRCGLHASSCEVALQ 180  
DB 121 LFOEYVGEDFWYIGLRDIDGRWEDGPAISLSISNSVYQCGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVLTP 188  
DB 181 WICEKVLTP 188

RESULT 3  
US-09-270-767-31816  
; Sequence 31816, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31816  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-31816

Query Match 5.2%; Score 54; DB 2; Length 189;  
Best Local Similarity 21.2%; Pred. No. 6.8e+02;  
Matches 18; Conservative 10; Mismatches 31; Indels 26; Gaps 3;

QY 22 SRWK-----VKAVLHRCVSYLWVALGLTITVILMSLLY-----Q 57  
DB 102 SKMKNLQPLDQIKDYFGAKVALYFAW--LGFYTMILRISVGVLCFLYGRITWNSDPIS 159

QY 58 RTLCCGSKGFMCSQCSRCPNLMNRN 82  
DB 160 RDICDDNGTINCPQCDRSCDYWRNLN 184

RESULT 4  
US-09-270-767-47033  
; Sequence 47033, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47033  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-47033

Query Match 5.2%; Score 54; DB 2; Length 189;  
Best Local Similarity 21.2%; Pred. No. 6.8e+02;  
Matches 18; Conservative 10; Mismatches 31; Indels 26; Gaps 3;

QY 22 SRWK-----VKAVLHRCVSYLWVALGLTITVILMSLLY-----Q 57  
DB 102 SKMKNLQPLDQIKDYFGAKVALYFAW--LGFYTMILRISVGVLCFLYGRITWNSDPIS 159

QY 58 RTLCCGSKGFMCSQCSRCPNLMNRN 82  
DB 160 RDICDDNGTINCPQCDRSCDYWRNLN 184

RESULT 5  
US-09-198-452A-1169



Sequence 1169, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Giffaie, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1169  
LENGTH: 189  
TYPE: PRF  
ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1169

Query Match 5.2%; Score 53.5; DB 2; Length 189;  
Best Local Similarity 33.3%; Pred. No. 7.7e+02;  
Matches 22; Conservative 10; Mismatches 21; Indels 13; Gaps 4;

QY 13 PAAPRQDDSRMNV-KAVLHRCVSYLVWV-----ALGLITVILMSLLYQRTLCGSGK 65  
DB 110 PPHPRDKMYRFEVLQAVIEILGLGVILVFDIIGCFPLFVAILLSLLY-----CNST 164

QY 66 GFMCSSQ 71  
DB 165 -FTCVQ 169

## RESULT 6

US-09-438-185A-761  
Sequence 761, Application US/09438185A  
Patent No. 6822071  
GENERAL INFORMATION:  
APPLICANT: Stephens, Richard  
APPLICANT: Mitchell, Wayne  
APPLICANT: Kalman, Sue  
APPLICANT: Davis, Ronald  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438,185A  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 60/108,279  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128,606  
PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 1074  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 761  
LENGTH: 188  
TYPE: PRF  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
OTHER INFORMATION: CPN0759  
US-09-438-185A-761

Query Match 4.9%; Score 50.5; DB 2; Length 188;  
Best Local Similarity 27.6%; Pred. No. 1.6e+03;  
Matches 21; Conservative 9; Mismatches 21; Indels 25; Gaps 4;

QY 89 FSNMGRD-----NNSSLK-----PCADKSHLTFPPNOGVNLF-----OEY 125  
DB 86 FSHKRGQVHGEIVTSLSEPLLLDLSPTFLIGGGLYSLFLENQVDRDFISHIKKY 145

QY 126 VGEDPYWIGLARDIDGM 141  
DB 146 AGDTFFPLSL-LETW 159

RESULT 7  
US-09-270-767-42805

Sequence 42805, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 42805  
LENGTH: 188  
TYPE: PRF  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-42805

Query Match 4.8%; Score 50; DB 2; Length 188;  
Best Local Similarity 21.3%; Pred. No. 1.8e+03;  
Matches 33; Conservative 16; Mismatches 48; Indels 58; Gaps 7;

QY 17 RVQDD-----SRWKVAVLHRCVSYLVWVAGLTVI-INSLLYQRTLCGSGKFGK 69  
DB 27 RKQDDKQDDTEGRWRKGLCVAVCTTNGQLVXDIXFIPKLSFLXY--FPGIXPRAPRC 84

QY 70 SQCSRCPNLMNRNHCYFYSMEKRDWNSLKFCA-----DKSHLTFPPNOGVNLF 124  
DB 85 S-----FSINLWY-----KWCATTLRKXKQILMKAPKSNWSVSQTSB 122

QY 125 YGEDPYWIGLARDIDGMWEDGPALSLTISNSV 159  
DB 123 -----PKLSAVCAITV 135

## RESULT 8

US-08-469-427A-5  
Sequence 5, Application US/08469427A  
Patent No. 5607918  
GENERAL INFORMATION:  
APPLICANT: Eriksson, Ulf  
APPLICANT: Olofsson, Birgitta  
APPLICANT: Aittalo, Kari  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,427A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 41979cp2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 5:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-5

Query Match      4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1

QY      149 LSLSTLSNSV--VOKCGTIRRCG 169
|||:::|||::|||
Db       56 LSMELMGNVVXQLVPSCVTVGRCG 79

RESULT 9
US-08-609-443B-5
Sequence 5, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PATJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

```

```

US-08-609-443B-5      TISSUE TYPE: adult mouse heart
Query Match           4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Cy    149 LSLSLNSV---YQKGTIHRG 169
      ||::|||::|||::|||
Db    56 LSMELMGVVVKQLVPSCVTYVRG 79

RESULT 10
US-08-569-063C-5
Sequence 5, Application US/08569063C
Patent No. 5828939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAUISOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-569-063C-5

Query Match           4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Cy    149 LSLSLNSV---YQKGTIHRG 169
      ||::|||::|||::|||
Db    56 LSMELMGVVVKQLVPSCVTYVRG 79

```



ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...188  
SEQUENCE DESCRIPTION: SEQ ID NO: 5087:  
US-09-107-433-5087

Query Match 4.6%; Score 47.5; DB 2; Length 188;  
Best Local Similarity 23.5%; Pred. No. 3.5e+03;  
Matches 19; Conservative 13; Mismatches 26; Indels 23; Gaps 4;

QY 88 YFSMEKRDWNSL-----KFC-----ADKSHLTFPDNQ-----GVNLFOEY 125  
DB 105 YF-LKQDAMSGFMTEVVRKICQLSPBERGLKQLSIITHLNEASQVALKSGFSLPRQF 163  
QY 126 VGEDFYWIGLRDIDGMRWEDG 146  
DB 164 KGSDDRYTRKMRDYLEFRYVKG 184

RESULT 14  
US-09-198-452A-135  
; Sequence 135, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffee, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 135  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-135

Query Match 4.6%; Score 47.5; DB 2; Length 189;  
Best Local Similarity 22.2%; Pred. No. 3.5e+03;  
Matches 22; Conservative 11; Mismatches 41; Indels 25; Gaps 5;

QY 64 SKGFMS-----QCSRCPN-----LMNRNGSHCYFSEMRD-WNSLKF---CA 104  
DB 89 ANNFYCKYFGDLAMCENKFCPLPHEGKITFWLR-----VOAEKKNIYVTLSLSDCAE 142  
QY 105 DKGSHLTFPDNQGVNLFOEYVGEDFYWIGLRDIDGMRW 143  
DB 143 EDCFYLRMRWELFGKLEKQADEHAWVALAQDLDGHAW 181

RESULT 15  
US-09-543-681A-7232  
; Sequence 7232, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7232  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7232

Query Match 4.5%; Score 47; DB 2; Length 188;  
Best Local Similarity 32.8%; Pred. No. 3.9e+03;  
Matches 19; Conservative 4; Mismatches 29; Indels 6; Gaps 3;

QY 55 LYQRTLCGSGKGFMSQCSRCP---NLMNRNG--SHCYF-FSMEKRDWNSLKFCAK 106  
DB 118 LLQKRSRFGKIFVACNYPPECQVLANKPINGECYCHYPLMEKRSQGVRLVCASK 175

Search completed: January 9, 2006, 15:38:01  
Job time : 26.2885 secs





```
OY 1 MADNSITSTLELPAAPRVODDSRWKXKAVLHAPCVSYLWVALGILTVILMSLLYQRTL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDVSIVSLELPTATQANDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWTL 60
OY 61 CCGSGFPGOSGSRCPNLMWRNGSHCYFSMEKRDMSLKFCAADGSHLTFPPNOGVN 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CCGSNYSTASCPSCDHRMKYGNHCYFSVEKDMNSLEFCLARDSHLVTITNQEMS 120
OY 121 LFEQYVGEDFWIGLRDIDGMRWEDGPALSLG-ILSNVYOKCGTTHRCGLHASSCEVAL 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 LQGVLFSEAFWICGLRNNGWMRWEDGSLNFSRISNSFVQTCGALINKGLQASSCEVPL 180
OY 180 QWICEKV 186
    |||:|||||
Db 181 HGVCKKV 187

RESULT 6
US-09-759-130B-83
; Sequence 83, Application US/09759130B
; Publication No. US2003002279A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-83

Query Match 15.4%; Score 159.5; DB 3; Length 188;
Best Local Similarity 25.5%; Pred. No. 8.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
OY 40 MVALGLTLVL-----MSLLT-----YQRTLCGS-----KGFMC 70
```

```
Db 5 MISSGLIVVLKVGWMTLFLLYFPQIFNKSNDGFTTTSYGVSQIFGSSSPSPNGFITT 64
OY 71 QC--SRCNLMWRNGSHCYFSMEKRDMSLKFCAADGSHLTFPPNOGVNLFQEVYGE 128
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 RSYGVTCFQDMEFYQARCFPLSTSSSWNEERDFCKGSGTLATVNTPEKLFELDDITDA 124
OY 129 DFYWTGL--RDIDGMRWEDGPALSLILSNVYOKCGTTHRCGL-----HASSCEVALQW 181
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 125 EKYTFGLYHHEBKRWKRNINNSVFNGVNTNONFNCAFI---GLTKTFDAASCDISYR 181
OY 182 ICEK 185
    |||:|||||
Db 182 ICEK 185

RESULT 7
US-10-741-790-83
; Sequence 83, Application US/10741790
; Publication No. US20040121396A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtel, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-535OMNIM
CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-790-83

Query Match 15.4%; Score 159.5; DB 4; Length 188;
Best Local Similarity 25.5%; Pred. No. 8.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
OY 40 MVALGLTLVL-----MSLLT-----YQRTLCGS-----KGFMC 70
```

```

Db      5 MISSLIYVVLKVGWMTLEFLYPQIFPKNSNGFTTTSXGVQSILFGSSSPSPNGFITTT    64
Oy      71 QC--SRCENLWMRNSHCYYFSMEKRDNWSLLKPCADKGSHLLTPPDNQGYNLFQEVYGE    128
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 RSYGVCPEDMEFYQARCFPLSTSSSNWESRDPCFKGKSTLAIVNTPEKLFLQDITDA    124
Oy      129 DFWYIGL---RIDIDWRMEDGPALESLSISNVQKCIHNCGL---HASSCEVALQW    181
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        125 EKYFIGHLHYHREKKRWMINNSVFNGVNTNONFNCAITI---GLTKTFDAASCDISYR    181
Oy      182 ICEK 185
        |||
Db      182 ICEK 185

RESULT 8
US-10-287-436A--69
; Sequence 69, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 69
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A--69

Query Match          15.4%; Score 159.5; DB 5; length 188;
Best Local Similarity 25.5%; Pred. No. 8,6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7

Oy      40 MVALLGLTYIL-----MSLLL-----YORTLCCGS-----KGFMC5 70
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      5 MISSLIYVVLKVGWMTLEFLYPQIFPKNSNGFTTTSXGVQSILFGSSSPSPNGFITTT    64
Oy      71 QC--SRCENLWMRNSHCYYFSMEKRDNWSLLKPCADKGSHLLTPPDNQGYNLFQEVYGE    128
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 RSYGVCPEDMEFYQARCFPLSTSSSNWESRDPCFKGKSTLAIVNTPEKLFLQDITDA    124
Oy      129 DFWYIGL---RIDIDWRMEDGPALESLSISNVQKCIHNCGL---HASSCEVALQW    181
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : ~~~~~
        125 EKYFIGHLHYHREKKRWMINNSVFNGVNTNONFNCAITI---GLTKTFDAASCDISYR    181
Oy      182 ICEK 185
        |||
Db      182 ICEK 185

RESULT 9
US-10-287-436A--1251
; Sequence 1251, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1251
```

```
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-436A-1251
```

```
Query Match          15.4%; Score 159.5; DB 5; Length 188;  
Best Local Similarity 25.5%; Pred. No. 8,6e-08;  
Matches    47; Conservative   31; Mismatches   65; Indels    41; Gaps      7
```

```
OY      40 MWALGLTVIL-----MSILL-----YORTLCGS--KGPMCS 70  
       |||::||  
DB      5 MISGLIVLVKVMQMTLFLLPQIFNKSNDFTTTSRYGVQSIFGSSSPNGFIYT 64  
OY      71 QC--SRCNLMNRNSHCYYFSMEKRDNSSLKFCADKSGSHLTTPDQGVLFGYEVC 128  
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB      65 RSYGVCPCKDMEFYQARCFPLSTSESSWNESRD FCGKGSTLAIVNTDEKLFDIDTA 124  
OY     129 DFWYIGL---RDIDGRMEDGPALSITLSNSVVQCGTIHRCGL---HASCEVALQM 181  
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB     125 EKTFGLHYHEBKRMKNINNVFNGVNTQNQNNCATI---GLTKTFAASCDISYR 181  
OY     182 ICEKV 185  
       |||  
DB     182 ICEK 185
```

```
RESULT 10  
US-09-764-870-487  
; Sequence 487, Application US/09764870  
; Patent No. US20020042386A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT14  
CURRENT APPLICATION NUMBER: US/09/764,870  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 646  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 487  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-764-870-487
```

```
Query Match          14.8%; Score 153.5; DB 3; Length 189;  
Best Local Similarity 27.2%; Pred. No. 3,5e-07;  
Matches    34; Conservative   25; Mismatches   61; Indels    5; Gaps      4
```

```
OY      64 SKGFMCSCC-SRCPMLMRNSHCYYFSMEKRDNSSLKFCADKSGSHLTTPDQGNVLF 122  
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB      65 SKG-CICCEACPDPDWLLYGRKCIFYEEEPDMWTGRQYCHTHEAVLAIVSQKELEFM 122  
OY     123 QEYGEDPYWVGIRD-I-DGMWMEDGPALSITLSNSVVQCGTIHRCGLHASCEVALQM 181  
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB     123 KFTFRRE-PWIGLRHVGEFFHWANGDDPDPTDTIAGEGECVFVEPTRLVSTECLMTRPW 181  
OY     182 ICEKV 186  
       :|||  
DB     182 VCSKM 186
```

```
RESULT 11  
US-10-125-540-487  
; Sequence 487, Application US/10125540  
; Publication No. US20030059675A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT14CI  
CURRENT APPLICATION NUMBER: US/10/125,540  
CURRENT FILING DATE: 2002-04-19  
Prior Application removed - See File Wrapper or Palm
```



NUMBER OF SEQ ID NOS: 646  
SOFTWARE: Patcentin Ver. 2.0  
SEQ ID NO 487  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-540-487

Query Match 14.8%; Score 153.5; DB 4; Length 189;  
Best Local Similarity 27.2%; Pred. No. 3.5e-07;  
Matches 34; Conservative 25; Mismatches 61; Indels 5; Gaps 4;

QY 64 SKGFMCSQC-SRCPNIMMANGSHCYFSEMEKRDMSLKFCADKSGHLLTFPDNGVNLF 122  
DB 65 SKG--CIRKCAPCPDMLLYGRKCYFSEBPDMDNGRQYCHTHEAVLAVIQSKLELFM 122  
QY 123 GSYVGEDFYWIGLRDI-DCMRWEDGPALSLSLNSVVKCGTIHRCGLHASCCEVALOM 181  
DB 123 FFFTRRE-FWIGLRVGVDFHVNQDPDPDPTTITAGPBCVVEPTRLVSTECMTTRFW 181  
QY 182 ICEKV 186  
DB 182 VCSKM 186

RESULT 12  
US-11-097-143-5490  
Sequence 5490, Application US/11097143  
Publication No. US20050208558A1  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
APPLICANT: et al.  
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
FILE REFERENCE: CL000728  
CURRENT APPLICATION NUMBER: US/11/097,143  
PRIOR FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: 60/157,832  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/160,191  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/161,932  
PRIOR FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: 60/164,769  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/173,383  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/175,693  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: 60/184,831  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/191,637  
PRIOR FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5490  
LENGTH: 188  
TYPE: PRT  
ORGANISM: DROSOPHILA  
US-11-097-143-5490

Query Match 8.3%; Score 92.5; DB 6; Length 188;  
Best Local Similarity 20.8%; Pred. No. 0.5;  
Matches 40; Conservative 29; Mismatches 68; Indels 55; Gaps 12;

QY 37 YLVMAVGLITVILMSLLYQRTLCGSKG-FMCSQCSRC-----PNLM-----MANGS 84  
DB 4 YLLSVI-----ISLQLCLDRTMAWTPPKGPGVADCPNVDSQYTPNKTWPLKLKGE 59  
QY 85 HCYYFSM-EKRDNNSSLKPCADKSGHLLTFPDNGVNLFOEYV-----GEDFYWIGLRDI 138  
DB 60 KRYYLGLFFKANNFKATQYCRYHGMHLASISSQEBNDRLKHTIDPGLGHEHFWISGIDL 119

QY 139 --DG---W-----RWEDGPALSLSLNSVVKCGTIHRC-----GH--HA 172  
DB 120 ADEGNPFWMATGRPTFTTNMAGE-----PNNFRYENGEBEENCLLELMNRDQGLKXMD 172  
QY 173 SSCEVALOWICE 184  
DB 173 SPCSFETYFVCE 184

RESULT 13  
US-11-097-143-3261  
Sequence 3261, Application US/11097143  
Publication No. US20050208558A1  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
APPLICANT: et al.  
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
FILE REFERENCE: CL000728  
CURRENT APPLICATION NUMBER: US/11/097,143  
PRIOR FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: 60/157,832  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/160,191  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/161,932  
PRIOR FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: 60/164,769  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/173,383  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/175,693  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: 60/184,831  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/191,637  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3261  
LENGTH: 188  
TYPE: PRT  
ORGANISM: DROSOPHILA  
US-11-097-143-3261

Query Match 7.3%; Score 75.5; DB 6; Length 188;  
Best Local Similarity 20.6%; Pred. No. 26;  
Matches 28; Conservative 27; Mismatches 50; Indels 31; Gaps 9;

QY 79 WMNGSHCYFYS-MEKRDNNSSLKPCADKSGHLLTFPDNGVNLFOEYV-----GEDFY 131  
DB 48 FVRIQDNYIIEPMNVKVNFFQAAGACRMNMAHLASIEDKPEMALIKYMAKGFKNNDYF 107  
QY 132 WIGLRDI--DG---WF-----WEDGPALSLSLNSVVKCGTIH-----RGLHA 172  
DB 108 WISGNDLGTGGAFYWMSNGRPMTYAPW-NGPKQMDPNYGN--ENC--VHMFATREMIWD 162

QY 173 SSCEVALOWICEKVP 188  
DB 163 ANCKIOMLYVCEATEP 178

RESULT 14  
US-10-114-893-48  
Sequence 48, Application US/10114893  
Publication No. US20020193567A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallie, Edward R.  
APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Bowman, Michael R.  
APPLICANT: Spaulding, Vikki  
APPLICANT: Carlin-Duckett, McKeough  
APPLICANT: Kelleher, Kerry S.  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: GI 6000-10A  
CURRENT APPLICATION NUMBER: US/10/114,893  
CURRENT FILING DATE: 2002-04-02  
EARLIER APPLICATION NUMBER: 09/413,232  
EARLIER FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 48  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-114-893-48

Query Match 7.3%; Score 75.5; DB 4; Length 189;  
Best Local Similarity 34.9%; Pred. No. 26;  
Matches 15; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

OY 70 SOCSR-CPNLMWRNGSHCYFPMERKDNNSLKFCADKSHLL 111  
DB 138 ANCSAPCFQDWIMHGNCYLFSGSGFPMWEKSEQECLSLDAKLL 180

RESULT 15  
US-10-424-599-250285  
Sequence 250285, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 250285  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_68035C.1.pep  
US-10-424-599-250285

Query Match 6.1%; Score 63.5; DB 4; Length 188;  
Best Local Similarity 24.5%; Pred. No. 4.3e+02;  
Matches 26; Conservative 15; Mismatches 36; Indels 29; Gaps 6;

OY 79 WMRNGSHCYFPMERKDNNS-----LKFGA---DKGSHLTFP-DNOGV---- 119  
DB 86 WHVDGHHFYVVGMDGGQSTSRSNYNLRDTSRCTVQVPRKWTAVVPLDVGMMNVR 145  
OY 120 --NLFOEYVGEDFYWIGLRDIDGMWEDGPALSLISNSVQKCG 163  
DB 146 SENMARIQYLGQQFYLGVSPPANSWRDE-----YPIPSNALV--CG 183

Search completed: January 9, 2006, 15:56:00  
Job time : 73.5381 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.6478 Seconds  
(without alignments)  
149.966 Million cell updates/sec

Title: US-09-811-367b-5  
Perfect score: 1036  
Sequence: 1 MADNSIYSTLELPAAPRVQD.....GLHASSCEVALQWICKVLP 188

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues  
Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188  
Maximum DB seq length: 189

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US05\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	188	US-10-055-877-206	Sequence 206, App
2	838	80.9	188	US-10-055-877-205	Sequence 205, App
3	545.5	52.7	189	US-10-055-877-207	Sequence 207, App
4	525.5	50.7	189	US-10-055-877-209	Sequence 209, App
5	45	4.3	188	US-10-467-657-245	Sequence 246, App
6	45	4.3	189	US-10-467-657-2690	Sequence 2690, App
7	44.5	4.1	188	US-10-131-826A-240	Sequence 240, App
8	42.5	4.0	188	US-10-945-853-2	Sequence 2, App
9	41	4.0	189	US-11-064-774A-117	Sequence 117, App
10	41	4.0	189	US-11-137-465-60	Sequence 60, App
11	40	3.9	188	US-10-1131-826A-232	Sequence 232, App
12	40	3.9	189	US-10-793-626-2976	Sequence 2976, App
13	40	3.9	189	US-10-793-626-2976	Sequence 3000, App
14	39.5	3.8	188	US-10-945-853-1	Sequence 1, App
15	39.5	3.8	189	US-11-147-492-10	Sequence 10, App
16	39	3.8	189	US-11-147-492-12	Sequence 12, App
17	39	3.8	189	US-11-147-492-16	Sequence 16, App
18	38	3.7	188	US-10-821-234-1393	Sequence 1393, App
19	38	3.7	188	US-10-528-031-4	Sequence 4, App
20	37.5	3.6	189	US-11-147-492-28	Sequence 28, App
21	37	3.6	189	US-11-147-492-10	Sequence 10, App
22	35	3.4	188	US-10-884-730-88	Sequence 88, App
23	35	3.4	189	US-10-467-657-4044	Sequence 4044, App
24	34.5	3.3	189	US-11-147-492-20	Sequence 20, App
25	34	3.3	189	US-11-147-492-26	Sequence 26, App

26	33.5	3.2	189	US-10-467-657-4524	Sequence 4524, App
27	33	3.2	189	US-10-995-551-643	Sequence 643, App
28	33	3.2	189	US-11-147-489-14	Sequence 14, App
29	32.5	3.1	188	US-11-036-797-37	Sequence 37, App
30	32.5	3.1	189	US-10-873-528-15	Sequence 15, App
31	32.5	3.1	189	US-10-873-528-15	Sequence 6, App
32	32.5	3.1	189	US-11-147-492-6	Sequence 18, App
33	32.5	3.1	189	US-11-147-492-18	Sequence 22, App
34	32	3.1	188	US-10-980-388-101	Sequence 101, App
35	32	3.1	188	US-11-147-492-8	Sequence 8, App
36	32	3.1	189	US-10-416-384-1	Sequence 1, App
37	31.5	3.0	188	US-10-884-730-294	Sequence 294, App
38	31.5	3.0	188	US-10-884-730-322	Sequence 322, App
39	31.5	3.0	188	US-10-485-517-221	Sequence 221, App
40	31	3.0	188	US-10-842-206-40	Sequence 40, App
41	31	3.0	188	US-10-980-459-32	Sequence 32, App
42	31	3.0	189	US-11-147-492-24	Sequence 24, App
43	30.5	2.9	189	US-10-467-657-3184	Sequence 3184, App
44	30	2.9	188	US-10-467-657-4400	Sequence 4400, App
45	30	2.9	188	US-10-467-657-7132	Sequence 7132, App

ALIGNMENTS

RESULT 1  
US-10-055-877-206  
; Sequence 206, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:  
; APPLICANT: Decristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zernhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eissen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055,877  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25

```

; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-055-877-206
```

```

Query Match          100.0%; Score 1036; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.7e-104;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1  MADNSIYSTLELPAAPRYVDDSRMKVKAVLHRCVSYLWVALGLITVILMSLLYORTL 60
        |||
DB      1  MADNSIYSTLELPAAPRYVDDSRMKVKAVLHRCVSYLWVALGLITVILMSLLYORTL 60
        |||
QY      61  CCGSKGFMCSCRCRCPNLMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPNOGVN 120
        |||
DB      61  CCGSKGFMCSCRCRCPNLMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPNOGVN 120
        |||
QY      121  LFGYVGEDFYWIGLRIDGWRMEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
        |||
DB      121  LFGYVGEDFYWIGLRIDGWRMEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
        |||
QY      181  WICKKVL 188
        |||
DB      181  WICKKVL 188
        |||

RESULT 2
US-10-055-877-205
; Sequence 205, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
```

```

; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 205
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-205
```

```

Query Match          80.9%; Score 838; DB 6; Length 188;
Best Local Similarity 80.7%; Pred. No. 3.2e-83;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```

```

QY      1  MADNSIYSTLELPAAPRYVDDSRMKVKAVLHRCVSYLWVALGLITVILMSLLYORTL 60
        |||
DB      1  MADNSIYSTLELPEAPVQDDSRMKVAVLHRCVSYLWVALGLITVILMSLLYORTL 60
        |||
QY      61  CCGSKGFMCSCRCRCPNLMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPNOGVN 120
        |||
DB      61  CCGSKDSTCHSCPILMTNNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPNOGVN 120
        |||
QY      121  LFGYVGEDFYWIGLRIDGWRMEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
        |||
DB      121  LFGYVGEDFYWIGLRIDGWRMEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
        |||
QY      181  WICKKVL 187
        |||
DB      181  WICKKVL 187
        |||

RESULT 3
US-10-055-877-207
; Sequence 207, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
```

```

APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eiben, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Verne, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacey
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262, 892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263, 598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263, 799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264, 117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263, 351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272, 870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275, 990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275, 927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 207
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
OS-10-055-877-207

```

Query Match	52.7%	Score 545.5	DB 6	length 189
Best Local Similarity	55.1%	Pred. No. 9.1e-52		
Matches	103	Conservative	28	Mismatches 55, Indels 1, Gaps 1
Qy	1	MADNSYSTLEIPAAPRVQDDSRMKVAVLHRCVSYLVMAVALLTVILMSLIYQRTL	60	
Db	1	MTDSVIYSMLLELPATQANDYGPQOKSSSPSCCIVAILAGLLTFLVLSVLLYQWIL	60	
Qy	61	CCGSAGFMCSCGSRCPNLMNRGSCYCFPSMEKRMNSLIRCADKSHLLTFPNQGVN	120	
Db	61	CGGSVYSTCASPSPDRMKYGNHCYFYSVEKUNSSLEFLARDSLHLLTIDNQMS	120	
Qy	121	LFQEVAGDEFYVIGLRDIDGMWEDEGPAISSLTSLTNSVYQKCGTIRCGLHASSCEVAL	179	
Db	121	LLQVFLSEAFCMVIGLRNNSGWRMEDGSPINPFRISISNPFVQCGAINKNGIASSCEVPL	180	
Qy	180	QWICEKV 186		
Db	181	HWCKKV 187		

```

Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Molenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
JS-10-055-877-209

```

Query Match	50.7%	Score 525.5	DB 6	Length 189
Best Local Similarity	53.5%	Pred. No. 1.3e-49		
Matches	100	Conservative	29	Mismatches 57; Indels 1; Gaps 1;

  

Qy	1	M	A	N	S	I	S	T	E	L	E	P	A	R	P	V	O	D	S	R	K	V	A	L	H	R	P	C	V	S	T	L	N	V	A	L	I	T	I	L	S	L	L	O	R	T	L		60							
Db	1	M	T	D	V	I	S	I	S	M	E	L	P	A	T	A	Q	N	D	I	Y	G	R	Q	K	S	S	S	P	C	S	C	L	V	A	I	T	I	O	L	I	T	R	A	V	L	S	V	L	I	Q	M	I	L		60

  

Qy	61	C	C	G	S	G	F	M	C	O	S	C	R	C	P	I	L	M	R	N	S	H	C	T	T	F	S	M	E	K	R	D	N	N	S	L	F	C	A	D	K	S	H	L	T	P	D	N	G	C	N		120
Db	61	C	C	G	S	G	F	M	C	O	S	C	R	C	P	I	L	M	R	N	S	H	C	T	T	F	S	M	E	K	R	D	N	N	S	L	F	C	A	D	K	S	H	L	T	P	D	N	G	C	N		120

Db 61 CGSNVSTCASCPCSDRMKYGKNCYFVSVEKDMNSSLBFCLARDSHLVTITNOEMS 120  
QY 121 LFEQVEVGEFFYVIGLRDIDGWRMEDGPAISLS-ILSNVYQKCGTTHRCGLHASSCEVAL 179  
Db 121 LQVLSLSEAFWCWIGLRNNSGWRMEDGSPLNFSRISNSFVQTCGALINNGLOASSCEVPL 180  
QY 180 GWICEKV 186  
Db 181 HGVCKKV 187

RESULT 5  
US-10-467-657-246  
Sequence 246, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACT Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 246  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-246

Query Match 4.3%; Score 45; DB 6; Length 189;  
Best Local Similarity 24.6%; Pred. No. 5.9e+02;  
Matches 16; Conservative 8; Mismatches 23; Indels 18; Gaps 4;  
QY 113 FPDNCGVNLFOEYVGEDEFWIG-----LRDIDGWRMEDGPAISLSILSNVYQKCGTTH 166  
Db 98 YPTN---NILDIFGARLWIPSETVAGILEKLDGKTEY-----LKNWYLRDAGGY- 146  
QY 167 RCGLH 171  
Db 147 -IGIH 150

RESULT 6  
US-10-467-657-2690  
Sequence 2690, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACT Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2690  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2690

Query Match 4.3%; Score 44.5; DB 6; Length 189;  
Best Local Similarity 20.1%; Pred. No. 6.6e+02;  
Matches 37; Conservative 25; Mismatches 47; Indels 75; Gaps 11;  
QY 28 AVLRPCVSYLVWVALGLTVILMSLLYQRTLCGSGKGFMCSCRCRPNLMRNGSHCY 87

Query Match 4.3%; Score 45; DB 6; Length 189;  
Best Local Similarity 24.6%; Pred. No. 5.9e+02;  
Matches 16; Conservative 8; Mismatches 23; Indels 18; Gaps 4;  
QY 113 FPDNCGVNLFOEYVGEDEFWIG-----LRDIDGWRMEDGPAISLSILSNVYQKCGTTH 166  
Db 98 YPTN---NILDIFGARLWIPSETVAGILEKLDGKTEY-----LKNWYLRDAGGY- 146  
QY 167 RCGLH 171  
Db 147 -IGIH 150

RESULT 7  
US-10-131-826A-240  
Sequence 240, Application US/10131826A  
Publication No. US20050245730A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P333081C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 240  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-131-826A-240

Query Match 4.3%; Score 44.5; DB 6; Length 189;  
Best Local Similarity 20.1%; Pred. No. 6.6e+02;  
Matches 37; Conservative 25; Mismatches 47; Indels 75; Gaps 11;  
QY 28 AVLRPCVSYLVWVALGLTVILMSLLYQRTLCGSGKGFMCSCRCRPNLMRNGSHCY 87

```
Db 2 ALLSRP-----ALTLILLMAV-----RCGE-----24
Qy 88 YESMEKRDMSLKFCADKSHLFPDNOGVNLFQEVGDFPVMGL---RDIDG-----140
Db 25 --QAQOTTBRAVLTKITRN--GVHKIDTYLMAADLDLG---GED---GLCQYKCSDSKRF 74
Qy 141 --WRWEDGPA-----LSLSILSNSVVOKCGTTH-----RCGLHASSCEVALQNI 182
Db 75 PRYGVKSPSPNCGSPLFCVHNLIGIPs---LTKCNQNDRCVETCGKSKNDCEBFQYC 131
Qy 183 CEKV 186
Db 132 LSKI 135

RESULT 8
US-10-945-853-2
; Sequence 2, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Sanicola-Nadel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; APPLICANT: Williams, Kevin
; TITLE OF INVENTION: CripTo-Specific Antibodies
; FILE REFERENCE: BGNAL17CEPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/11950
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/286,782
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/293,020
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/301,091
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/367,002
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-853-2

Query Match 4.1%; Score 42.5; DB 6; Length 188;
Best Local Similarity 27.9%; Pred. No. 1.1e+03;
Matches 19; Conservative 8; Mismatches 34; Indels 7; Gaps 2;

Qy 19 QDDSRMKVKAHLRPPCVSLVMVALGLTITLMSLLYQRTLC--GSKGFMCSQGRCPN 77
Db 47 RDSISIPQEBPARPRSSQSV-----LPMGIGHSKELNNTCTCLNGSTCWLBSFCACPFS 100
Qy 78 LWMRNGSH 85
Db 101 FYGRNCEH 108

RESULT 9
US-11-064-774A-117
; Sequence 117, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Ailtalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWT
; FILE REFERENCE: 28967/35977B2
```

```
; CURRENT APPLICATION NUMBER: US/11/064,774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-117

Query Match 4.0%; Score 41; DB 7; Length 188;
Best Local Similarity 31.6%; Pred. No. 1.6e+03;
Matches 6; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 151 LSILSNSVVOKCGTTHRCG 169
Db 61 MGTVAKQLVPSCVTVQRCG 79

RESULT 10
US-11-137-465-60
; Sequence 60, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahllick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GFS0018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-60

Query Match 4.0%; Score 41; DB 7; Length 189;
Best Local Similarity 35.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 144 EDGPALSLILSNSVVOKCG 163
Db 168 DDEHKMSVHYVNTSLVEXCG 187

RESULT 11
US-10-131-826A-232
; Sequence 232, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```

1  APPLICANT: Beresini, Maureen
2  APPLICANT: DeForge, Laura
3  APPLICANT: Deenoyers, Luc
4  APPLICANT: Flivaroff, Ellen
5  APPLICANT: Gao, Wei-Qiang
6  APPLICANT: Gerritsen, Mary E.
7  APPLICANT: Goddard, Audrey
8  APPLICANT: Godowski, Paul J.
9  APPLICANT: Gurney, Austin L.
10 APPLICANT: Sherwood, Steven
11 APPLICANT: Smith, Victoria
12 APPLICANT: Stewart, Timothy A.
13 APPLICANT: Tumas, Daniel
14 APPLICANT: Watanabe, Colin K
15 APPLICANT: Wood, William
16 APPLICANT: Zhang, Zemin
17 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
18 FILE OF INVENTION: ACIDS ENCODING THE SAME
19 FILE REFERENCE: P3330R1C128
20 CURRENT APPLICATION NUMBER: US/10/131,826A
21 CURRENT FILING DATE: 2002-04-24
22 PRIOR APPLICATION NUMBER: 60/049911
23 PRIOR FILING DATE: 1997-06-18
24 PRIOR APPLICATION NUMBER: 60/056974
25 PRIOR FILING DATE: 1997-08-26
26 PRIOR APPLICATION NUMBER: 60/059113
27 PRIOR FILING DATE: 1997-09-17
28 PRIOR APPLICATION NUMBER: 60/059115
29 PRIOR FILING DATE: 1997-09-17
30 PRIOR APPLICATION NUMBER: 60/059117
31 PRIOR FILING DATE: 1997-09-17
32 PRIOR APPLICATION NUMBER: 60/059122
33 PRIOR FILING DATE: 1997-09-17
34 PRIOR APPLICATION NUMBER: 60/059184
35 PRIOR FILING DATE: 1997-09-17
36 PRIOR APPLICATION NUMBER: 60/059263
37 PRIOR FILING DATE: 1997-09-18
38 PRIOR APPLICATION NUMBER: 60/059352
39 PRIOR FILING DATE: 1997-09-19
40 PRIOR APPLICATION NUMBER: 60/059588
41 PRIOR FILING DATE: 1997-09-19
42 REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
43 NUMBER OF SEQ ID NOS: 550
44 SEQ ID NO 232
45 LENGTH: 189
46 TYPE: PRT
47 ORGANISM: Homo Sapien
48 OS-10-131-826A-232

```

```

Query March_Similarity 3.9%; Score 40; DB 6; Length 189;
Best Local Similarity 19.3%; Pred. No. 2e+03;
Matches 31; Conservative 21; Mismatches 47; Indels 62; Gaps 8

Qy LGLTVIIMSLILYXO---RTLCGSK--GFMCQSQR--CPNLMWRNGSCYYFSMEKRD 95
|||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db LGSRAVMILLLLPWTAGRAVPGSGSPAWTQCQQLSQKLCTLAW---SAHPLVGHWDLRE 58

Qy -----WNSLKFCADKSKSHLLTFPDNGCVNLFGTYGEDPF- 131
|||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 59 EGDETTNDVPHIQGCGDGPQGLRDNDSQFCLQR-----IHQGLIFYEKLGLSDIFT 110

Qy 132 -----WIGLRDI---DCGRWEDGPALSLIS 152
||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 111 GPSPILPDSPYVGQLHASLIGLSQLLQPEGHMHTQQIPLSL 151

RESULT 12
US-10-793-626-2976
; Sequence 2976, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
```

```

? FILE REFERENCE: PU340US
? CURRENT APPLICATION NUMBER: US/10/793,626
? CURRENT FILING DATE: 2004-03-04
? PRIOR APPLICATION NUMBER: 60/164,258
? PRIOR FILING DATE: 1999-11-09
? NUMBER OF SEQ ID NOS: 4472
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2976
? LENGTH: 189
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: Description of Artificial Sequence: synthetic
? OTHER INFORMATION: amino acid sequence
US-10-793-626-2976

```

Query Match 3.9%; Score 40; DB 6; Length 189;  
 Best Local Similarity 30.6%; Pred. No. 2e+03;  
 Matches 11; Conservative 7; Mismatches 14; Indels 4; Gaps 1.

```

RESULT 13
US-10-793-626-3000
; Sequence 3000, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P13480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3000
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3000

```

```
Query Match          3.9% Score 40 ; DB 6; Length 189;  
Beet Local Similarity 30.6%; Pred. No. 2e+03;  
Matches 11; Conservative ?; Mismatches 14; Indels 4; Gaps 1  
  
Oy      115 DNOGVNLFOEYVGEDFYWIGLRDIDG---NRMBDG 146  
       |:|::||:||||:  
Db      145 DSEAVLQMNLTGHDFIFTRERDTGTSIVRRKDG 180  
  
RESULT 14  
US-10-945-853-1  
Sequence 1, Application US/10945853  
Publication NO. US20050255117A1  
GENERAL INFORMATION:  
APPLICANT: Biogen, Inc.  
APPLICANT: Sanicola-Nadel, Michele  
APPLICANT: Adkins, Heather  
APPLICANT: Miklaez, Steven Donald  
APPLICANT: Rayhorn, Paul  
APPLICANT: Schifter, Susan Gail  
APPLICANT: Williams, Kevin  
TITLE OF INVENTION: Cricko-Specific Antibodies  
FILE REFERENCE: BGNAL17CPRCN  
CURRENT APPLICATION NUMBER: US/10/945,853  
CURRENT FILING DATE: 2004-09-20
```





Handwritten text, possibly a signature or date, oriented vertically.